

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	8	AdQ16409 Amino acid
2	6	85.7	371	7	AdF04626 Bacterial
3	6	85.7	415	6	Adb08414 Allioococ
4	6	85.7	503	6	AdB08416 Allioococ
5	6	85.7	717	6	AdB08418 Allioococ
6	6	85.7	1526	4	Adb08419 Drosophil
7	5	71.4	8	2	Aav36486 Peptide #
8	5	71.4	8	3	AY88609 T-cell re
9	5	71.4	10	4	Aau25180 Beta-2-mi
10	5	71.4	10	4	AAU25775 Breast ca
11	5	71.4	21	9	ADU98146 mS101 cal
12	5	71.4	22	4	Aam17466 Peptide #
13	5	71.4	22	4	Adb336486 Peptide #
14	5	71.4	22	4	AAM29985 Peptide #
15	5	71.4	22	4	Abb31180 Peptide #
16	5	71.4	22	4	Abb21828 Protein #
17	5	71.4	22	4	AM63951 Human bone
18	5	71.4	22	4	AAM57249 Human brain
19	5	71.4	22	4	ABG51333 Human liver
20	5	71.4	22	4	AAM05144 Peptide #
21	5	71.4	22	4	ABG3971 Human pep
22	5	71.4	41	7	AdB81615 Human ova
23	5	71.4	45	8	ADS07258 Staphyloc

24	71.4	ADU79042 Human pco
25	5	ABP04426 Human ORF
26	5	ABC06841 Novel hum
27	5	ABP10817 Human ORF
28	5	AB066622 Klabsiell
29	5	Aan95241 Human rep
30	5	AB95938 Human tes
31	5	ABG06812 Novel hum
32	5	Aac71384 Human gen
33	5	ABG22770 Novel hum
34	5	ACu51061 Propionib
35	6	ABN59580 Propionib
36	5	ABG19849 Novel hum
37	5	ABP43071 Human ova
38	5	ADT05847 Plant ful
39	5	AB94957 Human pro
40	5	ABu0255 Human nov
41	5	ADR14686 Human NF
42	5	ADN87692 Human EST
43	5	Reu31384 Novel hum
44	5	AbD00449 Novel ova
45	5	Adx88163 Plant ful
46	5	AAG16191 Arabidops
47	5	Aau30881 Novel hum
48	5	AdG65762 Putative
49	5	AdG64647 Human pro
50	5	AdP58647 Human pol
51	5	Adm81098 Tumour-as
52	5	Ady05516 Plant ful
53	5	Adr90527 Human ret
54	5	AAG91093 C Glutami
55	5	Adr71964 Corynebac
56	5	Abd51881 Human sec
57	5	Adx76620 Plant ful
58	5	AdD26756 Human adi
59	5	AdS1880 Gene 2 hu
60	5	AAG13319 Arabidops
61	5	AbG66919 Murine Rb
62	5	Ady64822 S. manso
63	5	AAG53487 Arabidops
64	5	AdG08198 Arabidops
65	5	AdD21447 Mouse-ear
66	5	AdE61147 Thale cre
67	5	AdG27486 Arabidops
68	5	Abd43294 Protein e
69	5	AAG13318 Arabidops
70	5	AdE13835 Human lun
71	5	AdP39865 Staphyloc
72	5	AdD66701 Human lun
73	5	AdE59337 Human Pro
74	5	AdD45625 Human Pro
75	5	AdE87955 Human lun
76	5	AdS06905 Staphyloc
77	5	Adm81895 Tumour-as
78	5	AdS88276 Human pro
79	5	AAG53486 Arabidops
80	5	Aau17534 Novel SIG
81	5	AdD93819 Human nov
82	5	AdB94242 Human nov
83	5	Acr90533 Human ret
84	5	Adr90534 Arabidops
85	5	AdG08197 Arabidops
86	5	AdD26797 Human adi
87	5	AdN72128 Human NTR
88	5	AdB94242 Human nov
89	5	AdR90534 Arabidops
90	5	AAG27485 Human
91	5	Abd64552 Drosophil
92	5	Adw36516 Human syn
93	5	AAV41709 Human PRO
94	5	AdB40802 Human ORF
95	5	AdB44265 Human PRO
96	5	AdB24048 Human PRO

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	8	AdQ16409 Amino acid
2	6	85.7	371	7	AdF04626 Bacterial
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8	5	71.4	8	3	AY88609 T-cell re
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10	5	71.4	10	4	AAU25775 Breast ca
11	5	71.4	21	9	ADU98146 mS101 cal
12	5	71.4	22	4	Aam17466 Peptide #
13	5	71.4	22	4	Adb336486 Peptide #
14	5	71.4	22	4	AAM29985 Peptide #
15	5	71.4	22	4	Abb31180 Peptide #
16	5	71.4	22	4	Abb21828 Protein #
17	5	71.4	22	4	AM63951 Human bone
18	5	71.4	22	4	AAM57249 Human brain
19	5	71.4	22	4	ABG51333 Human liv
20	5	71.4	22	4	AAM05144 Peptide #
21	5	71.4	22	4	ABG3971 Human pep
22	5	71.4	41	7	AdB81615 Human ova
23	5	71.4	45	8	ADS07258 Staphyloc

97	5	71.4	224	4	AAB64539	Gene 45 h	170	71.4	224	9	ABD63934	Different	
98	5	71.4	224	4	AAB64466	Human sec	171	71.4	225	9	ABD59585	Human pol	
99	5	71.4	224	4	AAB65446	Human sec	172	5	71.4	225	9	ABM96257	M. xanthu
100	5	71.4	224	5	ABP03470	Human ORF	173	5	71.4	229	3	AAV74692	Neisseria
101	5	71.4	224	6	ABO22111	Novel hum	174	5	71.4	229	3	AAV74694	Neisseria
102	5	71.4	224	6	ABU72217	Novel hum	175	5	71.4	229	6	ABP79613	N. gonorr
103	5	71.4	224	6	ABU84897	Human sec	176	5	71.4	229	6	ABU37138	Protein e
104	5	71.4	224	6	ABU61095	Human PRO	177	5	71.4	229	6	ABU38067	Protein e
105	5	71.4	224	6	ABU610364	Human sec	178	5	71.4	231	2	AAB04747	Amnino aci
106	5	71.4	224	6	ADA24701	Novel hum	179	5	71.4	233	4	ABG22771	Novel hum
107	5	71.4	224	6	ABO19666	Novel hum	180	5	71.4	233	9	ABM95205	M. xanthu
108	5	71.4	224	6	ADA12362	Human sec	181	5	71.4	234	7	ADP30131	Bacterial
109	5	71.4	224	6	ABO19557	Novel hum	182	5	71.4	234	8	ADP44121	Plant ful
110	5	71.4	224	7	ADB73668	Human PRO	183	5	71.4	235	8	AAB04748	Amnino aci
111	5	71.4	224	7	ADB76384	Human PRO	184	5	71.4	240	3	AAB43978	Human can
112	5	71.4	224	7	ADC43810	Human sec	185	5	71.4	241	3	AAQ22776	Arabidops
113	5	71.4	224	7	ADC61570	Human sec	186	5	71.4	241	3	AAG27484	Arabidops
114	5	71.4	224	7	ADC63534	Human sec	187	5	71.4	242	8	ADP30131	Bacterial
115	5	71.4	224	7	ADC66534	Human sec	188	5	71.4	250	8	ADT72425	Plant ful
116	5	71.4	224	7	ADC68758	Human sec	189	5	71.4	254	5	AAY4165	Human che
117	5	71.4	224	7	ADC62818	Human sec	190	5	71.4	254	3	AAB10491	Human CXC
118	5	71.4	224	7	ADC67883	Human sec	191	5	71.4	254	3	AAB34731	Human sec
119	5	71.4	224	7	ADC61203	Human sec	192	5	71.4	254	4	AAB64423	Amnino aci
120	5	71.4	224	7	ADC67258	Human sec	193	5	71.4	254	4	AAB84199	Amnino aci
121	5	71.4	224	7	ADC62194	Human sec	194	5	71.4	254	5	AQ014627	Human SEA
122	5	71.4	224	7	ADC61127	Human sec	195	5	71.4	254	5	AAb84955	Human PRO
123	5	71.4	224	7	ADC62918	Human PRO	196	5	71.4	254	5	ABB95561	Human sca
124	5	71.4	224	7	ADC67883	Human PRO	197	5	71.4	254	3	ADD10567	Human sec
125	5	71.4	224	7	ADC61956	Human sec	198	5	71.4	254	7	ADD11527	Human sec
126	5	71.4	224	7	ADC67250	Human sec	199	5	71.4	254	7	ADD37320	Human sec
127	5	71.4	224	7	ADC62194	Human sec	200	5	71.4	254	7	ADG87435	Human SEA
128	5	71.4	224	7	ADD1297	Human sec	201	5	71.4	254	7	ADG87437	Human che
129	5	71.4	224	7	ADD72337	Human sec	202	5	71.4	254	7	ADZ51814	Human sca
130	5	71.4	224	7	ADD45142	Human PRO	203	5	71.4	254	8	ADP41528	Human sec
131	5	71.4	224	7	ADD51986	Human PRO	204	5	71.4	254	8	ADH43711	Human PRO
132	5	71.4	224	7	ADD49196	Human sec	205	5	71.4	254	8	ADK83056	Human PRO
133	5	71.4	224	7	ADE31250	Human sec	206	5	71.4	258	6	AD35702	Acinetob
134	5	71.4	224	7	ADD16364	Human sec	207	5	71.4	261	4	ABD70543	Human PRO
135	5	71.4	224	7	ADD12979	Human sec	208	5	71.4	261	6	ABD001372	Human pro
136	5	71.4	224	7	ADD1988	Human sec	209	5	71.4	261	6	ABD001373	Human pro
137	5	71.4	224	7	ADD47002	Human sec	210	5	71.4	261	6	ABD001366	Human pro
138	5	71.4	224	7	ADG52759	Human sec	211	5	71.4	261	8	ADN96118	Human NOV
139	5	71.4	224	7	ADG60079	Human sec	212	5	71.4	261	8	ADN96104	Human NOV
140	5	71.4	224	7	ADG160839	Human sec	213	5	71.4	261	8	ADN96116	Human NOV
141	5	71.4	224	8	ADE48496	Human sec	214	5	71.4	263	5	ABP39793	Staphyloc
142	5	71.4	224	8	ADP89597	Human sec	215	5	71.4	263	8	ADP05572	Staphyloc
143	5	71.4	224	8	ADD161237	Human sec	216	5	71.4	273	3	AAV57907	Human tra
144	5	71.4	224	8	ADP61237	Human sec	217	5	71.4	273	4	AAV5095	Human pro
145	5	71.4	224	8	ADP39229	Human sec	218	5	71.4	273	4	AAm93986	Human sto
146	5	71.4	224	8	ADP45725	Human sec	219	5	71.4	273	6	ABD08260	Human che
147	5	71.4	224	8	ADP24121	Human sec	220	5	71.4	273	8	ADT75419	Marker ge
148	5	71.4	224	8	ADP48953	Human sec	221	5	71.4	273	8	ADG59517	Human myo
149	5	71.4	224	8	ADP23497	Human sec	222	5	71.4	275	8	ADP05917	Human tra
150	5	71.4	224	8	ADP3480	Human sec	223	5	71.4	275	8	ADU00280	Epoxide h
151	5	71.4	224	8	ADP26947	Human sec	224	5	71.4	279	4	AAV72625	Human ang
152	5	71.4	224	8	ADP22583	Human sec	225	5	71.4	290	7	ABD69586	Pseudomon
153	5	71.4	224	8	ADP41177	Human sec	226	5	71.4	291	6	ABP71288	Common re
154	5	71.4	224	8	ADP25222	Human sec	227	5	71.4	297	6	ABP70972	Epoxide h
155	5	71.4	224	8	ADP26123	Human sec	228	5	71.4	302	6	ADP07626	Alloioc
156	5	71.4	224	8	ADP34112	Human sec	229	5	71.4	303	6	ABP71291	Mouse the
157	5	71.4	224	8	ADP46349	Human sec	230	5	71.4	304	3	ABD26915	Drosophil
158	5	71.4	224	8	ADG50335	Human sec	231	5	71.4	306	4	ABD69724	Drosophil
159	5	71.4	224	8	ADG62359	Human sec	232	5	71.4	302	3	ABD15108	Protein e
160	5	71.4	224	8	ADH22384	Human neu	233	5	71.4	302	6	AAG72968	Human olf
161	5	71.4	224	8	ADM17161	Human sec	234	5	71.4	302	6	ABD07628	Alloiococ
162	5	71.4	224	8	ADL06595	Human sec	235	5	71.4	314	6	ABD26594	Protein e
163	5	71.4	224	8	ADL91853	Human PRO	236	5	71.4	314	6	ABD69724	Drosophil
164	5	71.4	224	8	ADP54173	Human PRO	237	5	71.4	314	6	ABD15108	Protein e
165	5	71.4	224	8	ADT91094	Human PRO	238	5	71.4	310	6	AAG72968	Human olf
166	5	71.4	224	8	ADU50117	PRO615, S	239	5	71.4	312	4	ABP75962	Human sec
167	5	71.4	224	9	ADW49396	PRO615, pr	240	5	71.4	314	6	ABD35598	Acinotoba
168	5	71.4	224	9	ADZ252057	Human sec	241	5	71.4	314	6	ABD71289	Mouse the
169	5	71.4	224	9	AED47885	Human PRO	242	5	71.4	320	6	ABP71289	Mouse the

Result No.	Query Match	Length	DB ID	Description
1	6 85.7	87 4	US-10-425-115-291176	Sequence 291176, Sequence 224207, Sequence 2354, AP
2	6 85.7	119 4	US-10-425-115-224207	Sequence 55, AP
3	6 85.7	415 5	US-10-501-282-2354	Sequence 18609, AP
4	6 85.7	503 5	US-10-501-282-2356	Sequence 2358, AP
5	6 85.7	717 5	US-10-501-282-2358	Sequence 47, AP
6	6 85.7	1375 3	US-09-808-602-66	Sequence 66, AP
7	6 85.7	1375 3	US-09-800-198-55	Sequence 104, AP
8	6 85.7	1526 6	US-11-097-143-18609	Sequence 253500, AP
9	5 71.4	10 3	US-09-827-345-8	Sequence 6553, AP
.10	5 71.4	10 4	US-10-227-616-47	Sequence 283377, AP
11	5 71.4	10 6	US-11-220-407-8	Sequence 8, AP
12	5 71.4	22 3	US-09-844-761-37126	Sequence 37126, AP
13	5 71.4	41 5	US-10-481-561-104	Sequence 104, AP
14	5 71.4	42 4	US-10-425-115-253500	Sequence 253500, AP
15	5 71.4	45 4	US-10-425-115-283377	Sequence 6553, AP
16	5 71.4	45 4	US-10-425-115-241966	Sequence 241966, AP
17	5 71.4	50 4	US-10-425-115-241966	Sequence 415, AP
18	5 71.4	50 5	US-10-776-013-415	Sequence 206558, AP
19	5 71.4	51 4	US-10-424-599-206558	Sequence 215732, AP
20	5 71.4	53 4	US-10-425-115-215732	Sequence 129824, AP
21	5 71.4	55 4	US-10-437-963-129824	Sequence 311628, AP
22	5 71.4	55 4	US-10-425-115-311628	Sequence 204269, AP
23	5 71.4	56 4	US-10-437-963-204269	Sequence 204269, AP
24	5 71.4	64 5	US-10-450-763-37200	Sequence 37200, AP
25	5 71.4	66 4	US-10-435-115-18844	Sequence 18844, AP
26	5 71.4	66 4	US-10-425-115-221947	Sequence 221947, AP
27	5 71.4	67 4	US-10-425-115-211727	Sequence 211727, AP

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:20:08 ; Search time 186 Seconds  
(without alignments)  
17.433 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2072432

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Listing first 1000 summaries

Database : Published Applications AA\_Main:\*

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3: /EMC\_Celerra\_SIDS3/\_prodata/2/\_pubpaa/\_US09\_PUBCOMB\_pep:\*

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6: /EMC\_Celerra\_SIDS3/\_prodata/2/\_pubpaa/\_US11\_PUBCOMB\_pep:\*

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### SUMMARIES

Result No. Score Query Match Length DB ID Description

1 6 85.7 87 4 US-10-425-115-291176 Sequence 291176, Sequence 224207, Sequence 2354, AP

2 6 85.7 119 4 US-10-425-115-224207 Sequence 55, AP

3 6 85.7 415 5 US-10-501-282-2354 Sequence 2356, AP

4 6 85.7 503 5 US-10-501-282-2356 Sequence 2358, AP

5 6 85.7 717 5 US-10-501-282-2358 Sequence 66, AP

6 6 85.7 1375 3 US-09-808-602-66 Sequence 55, AP

7 6 85.7 1375 3 US-09-800-198-55 Sequence 18609, AP

8 6 85.7 1526 6 US-11-097-143-18609 Sequence 8, AP

9 5 71.4 10 3 US-09-827-345-8 Sequence 47, AP

.10 5 71.4 10 4 US-10-227-616-47 Sequence 47, AP

11 5 71.4 10 6 US-11-220-407-8 Sequence 8, AP

12 5 71.4 22 3 US-09-844-761-37126 Sequence 37126, AP

13 5 71.4 41 5 US-10-481-561-104 Sequence 104, AP

14 5 71.4 42 4 US-10-425-115-253500 Sequence 253500, AP

15 5 71.4 45 4 US-10-724-972A-6553 Sequence 6553, AP

16 5 71.4 45 4 US-10-425-115-283377 Sequence 283377, AP

17 5 71.4 50 4 US-10-425-115-241966 Sequence 241966, AP

18 5 71.4 50 5 US-10-776-013-415 Sequence 415, AP

19 5 71.4 51 4 US-10-424-599-206558 Sequence 206558, AP

20 5 71.4 53 4 US-10-425-115-215732 Sequence 215732, AP

21 5 71.4 55 4 US-10-437-963-129824 Sequence 129824, AP

22 5 71.4 55 4 US-10-425-115-311628 Sequence 311628, AP

23 5 71.4 56 4 US-10-437-963-204269 Sequence 204269, AP

24 5 71.4 64 5 US-10-450-763-37200 Sequence 37200, AP

25 5 71.4 66 4 US-10-435-115-18844 Sequence 18844, AP

26 5 71.4 66 4 US-10-425-115-221947 Sequence 221947, AP

27 5 71.4 67 4 US-10-425-115-211727 Sequence 211727, AP

28 5 71.4 71.4 5 US-10-425-115-335848 Sequence 325848, AP

29 5 71.4 71.4 5 US-10-424-599-162307 Sequence 337261, AP

30 5 71.4 71.4 5 US-10-425-115-260249 Sequence 260249, AP

31 5 71.4 71.4 5 US-10-425-115-262526 Sequence 262526, AP

32 5 71.4 71.4 5 US-10-425-115-251146 Sequence 251146, AP

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37 5 71.4 71.4 5 US-10-425-115-305630 Sequence 305630, AP

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43 5 71.4 83 5 US-10-425-115-318800 Sequence 318800, AP

44 5 71.4 85 5 US-10-425-115-289659 Sequence 289659, AP

45 5 71.4 89 5 US-10-423-115-245717 Sequence 245717, AP

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58 5 71.4 108 4 US-10-425-115-353035 Sequence 353035, AP

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60 5 71.4 112 4 US-10-437-963-16431 Sequence 16431, AP

61 5 71.4 112 4 US-10-425-115-313801 Sequence 313801, AP

62 5 71.4 114 4 US-10-424-593-17936 Sequence 17936, AP

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64 5 71.4 117 4 US-10-425-115-219911 Sequence 219911, AP

65 5 71.4 117 4 US-10-425-115-315802 Sequence 315802, AP

66 5 71.4 118 4 US-10-425-115-236283 Sequence 236283, AP

67 5 71.4 119 4 US-10-425-115-302847 Sequence 302847, AP

68 5 71.4 120 4 US-10-264-049-40303 Sequence 40303, AP

69 5 71.4 120 4 US-10-425-114-61662 Sequence 61662, AP

70 5 71.4 122 4 US-10-425-115-316628 Sequence 316628, AP

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73 5 71.4 126 4 US-10-425-115-336605 Sequence 336605, AP

74 5 71.4 126 4 US-10-425-115-316667 Sequence 316667, AP

75 5 71.4 127 4 US-10-425-115-2833489 Sequence 2833489, AP

76 5 71.4 129 4 US-10-425-115-889-757 Sequence 757, AP

77 5 71.4 129 4 US-10-425-115-201349 Sequence 201349, AP

78 5 71.4 131 4 US-10-112-944-785 Sequence 785, AP

79 5 71.4 131 4 US-10-425-115-326604 Sequence 326604, AP

80 5 71.4 132 4 US-10-425-115-552-468 Sequence 552, AP

81 5 71.4 132 4 US-10-425-114-50827 Sequence 50827, AP

82 5 71.4 132 4 US-10-425-115-889-757 Sequence 757, AP

83 5 71.4 133 4 US-10-425-115-236726 Sequence 236726, AP

84 5 71.4 134 4 US-10-425-115-316688 Sequence 316688, AP

85 5 71.4 135 4 US-10-425-115-318470 Sequence 318470, AP

86 5 71.4 136 4 US-10-425-115-242282 Sequence 242282, AP

87 5 71.4 137 4 US-10-425-114-613331 Sequence 613331, AP

88 5 71.4 138 4 US-10-437-963-189336 Sequence 189336, AP

89 5 71.4 139 4 US-10-425-115-22139 Sequence 22139, AP

90 5 71.4 141 4 US-10-425-115-191446 Sequence 191446, AP

91 5 71.4 146 4 US-10-425-115-24488 Sequence 24488, AP

92 5 71.4 146 4 US-10-425-114-613331 Sequence 613331, AP

93 5 71.4 146 4 US-11-072-512-242282 Sequence 242282, AP

94 5 71.4 151 3 US-09-738-125-4847 Sequence 4847, AP

95 5 71.4 151 3 US-10-425-115-316822 Sequence 316822, AP

96. 5 71.4 154 4 US-10-425-115-24488 Sequence 24488, AP

97 5 71.4 155 4 US-10-437-963-204269 Sequence 204269, AP

98 5 71.4 155 4 US-10-450-763-37200 Sequence 37200, AP

99 5 71.4 156 4 US-10-435-115-18844 Sequence 18844, AP

100 5 71.4 162 4 US-10-425-114-5986 Sequence 45986, AP

101 5 71.4 162 4 US-10-425-115-246072 Sequence 246072, AP

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122	5	71.4	197	5	US-10-732-923-20317	Sequence 20317,	195	5	224	4	US-10-145-092A-162	Sequence 162, App
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168	5	71.4	224	4	US-10-166-709A-162	Sequence 162,	241	5	224	4	US-10-40-223-090-278	Sequence 162, App
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171	5	71.4	224	4	US-10-002-967A-162	Sequence 162,	244	5	224	4	US-10-223-089-278	Sequence 162, App
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5	32	86.5	312	7	Sequence 37814, A
6	32	86.5	312	7	Sequence 105317,
7	32	86.5	312	7	Sequence 116316,
8	32	86.5	928	7	Sequence 8, Appl1
9	32	86.5	928	7	Sequence 8, Appl1
10	32	86.5	928	7	Sequence 8, Appl1
11	30	81.1	89	6	Sequence 50568, A
12	30	81.1	303	6	Sequence 30928, A
13	30	81.1	563	6	Sequence 43710, A
14	30	81.1	563	6	Sequence 53414, A
15	30	81.1	1013	6	Sequence 45687, A
16	29	78.4	218	7	Sequence 91402, A
17	29	78.4	218	7	Sequence 95158, A
18	29	78.4	222	7	Sequence 91401, A
19	29	78.4	222	7	Sequence 95157, A
20	29	78.4	228	7	Sequence 91400, A
21	29	78.4	228	7	Sequence 95156, A
22	29	78.4	293	6	Sequence 17, Appl1
23	29	78.4	324	7	Sequence 7912, Appl1
24	29	78.4	403	6	Sequence 553, Appl1
25	29	78.4	403	6	Sequence 3752, Appl1
26	29	78.4	403	6	Sequence 10-953-349-3752
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29	28	75.7	328	7	US-11-330-403-6440
30	28	75.7	370	6	US-10-505-928-772
31	28	75.7	386	6	US-10-953-349-21708
32	28	75.7	386	7	US-11-056-355B-65831
33	28	75.7	493	6	US-11-953-349-8397
34	28	75.7	661	7	US-11-320-072-92
35	28	75.7	706	7	US-11-793-697-3919
36	28	75.7	747	7	US-11-056-355B-86580
37	28	75.7	756	7	US-11-293-697-7722
38	28	75.7	758	6	US-11-774-894-171
39	28	75.7	765	7	US-11-056-355B-882533
40	28	75.7	777	7	US-11-056-355B-86579
41	28	75.7	795	7	US-11-056-355B-82532
42	28	75.7	815	6	US-10-449-902-44720
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53	27	73.0	178	7	Sequence 15591, A
54	27	73.0	178	7	Sequence 352698
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56	27	73.0	180	7	Sequence 52697, A
57	27	73.0	180	7	Sequence 20470, A
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66	27	73.0	232	6	Sequence 15589
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69	27	73.0	335	7	Sequence 9515, A
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71	27	73.0	395	7	Sequence 31936, A
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87	27	73.0	444	7	Sequence 31934, A
88	27	73.0	444	7	Sequence 33087, A
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91	27	73.0	444	7	Sequence 115161, A
92	27	73.0	490	7	Sequence 1587, A
93	27	73.0	533	6	Sequence 10-449-902-30801
94	27	73.0	533	6	Sequence 33087, A
95	27	73.0	535	7	US-11-056-355B-115656
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97	27	73.0	591	6	US-10-449-902-56603
98	27	73.0	599	7	US-10-293-697-2702

99	27	73.0	600	6	US-10-449-902-55351	Sequence 55351, A	Sequence 174, App
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101	27	73.0	845	7	US-11-056-355B-71216	Sequence 71216, A	Sequence 94727, A
102	27	73.0	880	7	US-11-330-403-3453	Sequence 3453, App	Sequence 313, App
103	27	73.0	897	7	US-11-056-355B-71215	Sequence 71215, A	Sequence 118, App
104	27	73.0	912	7	US-11-056-355B-71214	Sequence 71214, A	Sequence 121, App
105	27	73.0	1180	6	US-10-449-902-41079	Sequence 41079, A	Sequence 2988, App
106	27	73.0	1252	6	US-10-511-302A-42	Sequence 42, App1	Sequence 16, App1
107	27	73.0	1259	6	US-10-543-503-134	Sequence 134, App	Sequence 3261, App
108	26	70.3	112	7	US-11-232-41-112	Sequence 12, App1	Sequence 180, App
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113	26	70.3	173	7	US-11-192-046-74	Sequence 74, App1	Sequence 186, App
114	26	70.3	173	7	US-11-192-046-93	Sequence 93, App1	Sequence 187, App
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122	26	70.3	242	6	US-10-560-299-7	Sequence 7, Appli	Sequence 195, App
123	26	70.3	243	6	US-10-551-236-4	Sequence 4, Appli	Sequence 196, App
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126	26	70.3	294	6	US-11-434-137-9880	Sequence 9880, App	Sequence 199, App
127	26	70.3	290	7	US-11-434-184-9880	Sequence 9880, App	Sequence 200, App
128	26	70.3	290	7	US-11-434-199-9880	Sequence 9880, App	Sequence 201, App
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133	26	70.3	307	7	US-11-434-199-2758	Sequence 2758, App	Sequence 206, App
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135	26	70.3	311	6	US-10-417-571A-2418	Sequence 2418, App	Sequence 208, App
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138	26	70.3	326	7	US-11-056-355B-55527	Sequence 53527, A	Sequence 211, App
139	26	70.3	326	7	US-10-449-902-36632	Sequence 36632, A	Sequence 212, App
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141	26	70.3	384	6	US-10-449-902-40368	Sequence 40368, A	Sequence 214, App
142	26	70.3	385	7	US-11-056-355B-9382	Sequence 9382, App	Sequence 215, App
143	26	70.3	386	7	US-11-434-111-92	Sequence 92, App1	Sequence 216, App
144	26	70.3	392	6	US-10-953-349-16559	Sequence 16559, A	Sequence 217, App
145	26	70.3	392	6	US-11-056-355B-55525	Sequence 53525, A	Sequence 223, App
146	26	70.3	407	6	US-10-449-902-28633	Sequence 28633, A	Sequence 224, App
147	26	70.3	418	6	US-11-449-902-35339	Sequence 35339, A	Sequence 225, App
148	26	70.3	428	6	US-10-449-902-44039	Sequence 44039, A	Sequence 227, App
149	26	70.3	441	6	US-10-953-349-16558	Sequence 16558, A	Sequence 228, App
150	26	70.3	441	7	US-11-056-355B-55525	Sequence 53525, A	Sequence 229, App
151	26	70.3	449	7	US-11-056-355B-36684	Sequence 36684, A	Sequence 230, App
152	26	70.3	449	7	US-11-056-355B-104960	Sequence 104960, A	Sequence 231, App
153	26	70.3	449	7	US-11-056-355B-116199	Sequence 116199, A	Sequence 232, App
154	26	70.3	449	7	US-11-449-902-44084	Sequence 4084, App	Sequence 233, App
155	26	70.3	454	6	US-10-953-349-2364	Sequence 2364, App	Sequence 234, App
156	26	70.3	465	6	US-10-449-902-36079	Sequence 36079, A	Sequence 235, App
157	26	70.3	468	7	US-11-330-403-1925	Sequence 1925, App	Sequence 236, App
158	26	70.3	472	6	US-10-669-920-1418	Sequence 1418, App	Sequence 237, App
159	26	70.3	481	6	US-10-449-902-53990	Sequence 53990, A	Sequence 238, App
160	26	70.3	490	6	US-10-449-902-56644	Sequence 56644, A	Sequence 239, App
161	26	70.3	494	6	US-10-953-349-2363	Sequence 2363, App	Sequence 240, App
162	26	70.3	496	7	US-11-056-355B-90973	Sequence 90973, A	Sequence 241, App
163	26	70.3	496	7	US-11-056-355B-94729	Sequence -94729, A	Sequence 242, App
164	26	70.3	500	7	US-11-234-195-6	Sequence 6, Appli	Sequence 8, Appli
165	26	70.3	533	7	US-11-056-355B-9381	Sequence 9381, App	Sequence 5, Appli
166	26	70.3	594	6	US-10-449-902-52039	Sequence 52090, A	Sequence 38085, A
167	26	70.3	595	6	US-10-449-902-38085	Sequence 38085, A	Sequence 4825, App
168	26	70.3	611	7	US-11-293-697-4318	Sequence 4318, App	Sequence 5998, App
169	26	70.3	619	6	US-10-449-902-56241	Sequence 56241, App	Sequence 5998, App
170	26	70.3	677	7	US-11-056-355B-94728	Sequence 90972, A	Sequence 5998, App
171	26	70.3	677	7	US-11-434-195-5198	Sequence 94729, A	Sequence 5998, App

Result No.	Score	Query	Match	Length	DB	ID	Description
1	37	100.0	7	8	ADQ16409		Adq16409 Amino aci
2	33	89.2	331	8	ADN18451		Adn18451 Bacterial
3	33	89.2	371	7	ADP04626		Adp04626 Bacterial
4	33	89.2	415	6	ADB08414		Adb08414 Alloioecoc
5	33	89.2	503	6	ADB08416		Adb08416 Alloioecoc
6	33	89.2	717	6	ADB08418		Adb08418 Alloioecoc
7	32	86.5	110	8	ADR0527		Adr0527 Human ret
8	32	86.5	172	4	AAB6919		Aab6919 Murine Rb
9	32	86.5	200	8	ADR0533		Adr0533 Human ret
10	32	86.5	207	8	ADB90538		Adb90538 Human ret
11	32	86.5	208	8	ADR0532		Adr0532 Human ret
12	32	86.5	264	3	AAG42941		Aag42941 Arabidopsis
13	32	86.5	264	3	AAG05410		Aag05410 Arabidopsis
14	32	86.5	264	8	ADT56245		Adt56245 Plant pol
15	32	86.5	312	3	AAG42940		Aag42940 Arabidopsis
16	32	86.5	312	3	AAG05409		Aag05409 Arabidopsis
17	32	86.5	781	2	AAB69369		Aab69369 Modified
18	32	86.5	781	6	ABU58794		Abu58794 Human ret
19	32	86.5	816	1	AAP82112		Aap82112 Human ret
20	32	86.5	816	2	AAR3564		Aar3564 Retinobla
21	32	86.5	816	2	AAR56568		Aar56568 Human ret
22	32	86.5	816	2	AAW71355		Aaw71355 Protein s
23	32	86.5	816	2	AAV01542		Aav01542 Human ret

Pred. No. is the number of results predicted by a chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	37	100.0	7	8	ADQ16409		Adq16409 Amino aci
2	33	89.2	331	8	ADN18451		Adn18451 Bacterial
3	33	89.2	371	7	ADP04626		Adp04626 Bacterial
4	33	89.2	415	6	ADB08414		Adb08414 Alloioecoc
5	33	89.2	503	6	ADB08416		Adb08416 Alloioecoc
6	33	89.2	717	6	ADB08418		Adb08418 Alloioecoc
7	32	86.5	110	8	ADR0527		Adr0527 Human ret
8	32	86.5	172	4	AAB6919		Aab6919 Murine Rb
9	32	86.5	200	8	ADR0533		Adr0533 Human ret
10	32	86.5	207	8	ADB90538		Adb90538 Human ret
11	32	86.5	208	8	ADR0532		Adr0532 Human ret
12	32	86.5	264	3	AAG42941		Aag42941 Arabidopsis
13	32	86.5	264	3	AAG05410		Aag05410 Arabidopsis
14	32	86.5	264	8	ADT56245		Adt56245 Plant pol
15	32	86.5	312	3	AAG42940		Aag42940 Arabidopsis
16	32	86.5	312	3	AAG05409		Aag05409 Arabidopsis
17	32	86.5	781	2	AAB69369		Aab69369 Modified
18	32	86.5	781	6	ABU58794		Abu58794 Human ret
19	32	86.5	816	1	AAP82112		Aap82112 Human ret
20	32	86.5	816	2	AAR3564		Aar3564 Retinobla
21	32	86.5	816	2	AAR56568		Aar56568 Human ret
22	32	86.5	816	2	AAW71355		Aaw71355 Protein s
23	32	86.5	816	2	AAV01542		Aav01542 Human ret

97	3.2	928	10	AER64206	Human ret	Aef64206	Human ret	170	29	78.4	224	
98	86.5	970	1	AAP9599	Human ret	Aap9599	Human ret	171	29	78.4	224	
99	6.6	66	4	ANU9143	Propionib	Aau9143	Propionib	172	29	78.4	224	
100	3.1	83.8	6.6	ABM45662	Propionib	Abm45662	Propionib	173	29	78.4	224	
101	3.1	83.8	128	4	ABG02275	Novel	Abg02275	Novel	174	29	78.4	224
102	3.1	83.8	224	3	AAB80802	Human ORF	Abp0802	Human ORF	175	29	78.4	224
103	3.1	83.8	224	5	ABP03470	Human ORF	Abp03470	Human ORF	176	29	78.4	224
104	3.1	83.8	339	6	ABU7118	Protein e	Abu7118	Protein e	177	29	78.4	224
105	3.1	83.8	361	6	ADA16646	Acinetob	Ada36646	Acinetob	178	29	78.4	224
106	3.1	83.8	508	8	ADQ67799	Novel	Adq67799	Novel	179	29	78.4	224
107	3.1	83.8	549	7	ABD79802	Pseudomon	Abd79802	Pseudomon	180	29	78.4	224
108	3.1	83.8	562	5	ABP73802	Candida a	Abp73802	Candida a	181	29	78.4	224
109	3.1	83.8	714	4	AAG70834	C albican	Aag70834	C albican	182	29	78.4	224
110	3.1	83.8	776	4	AAU61553	Propionib	Aau61553	Propionib	183	29	78.4	224
111	3.1	83.8	776	6	ABR38072	Propionib	Abm38072	Propionib	184	29	78.4	224
112	3.1	83.8	1047	4	ABB67483	Drosophil	Abb67483	Drosophil	185	29	78.4	224
113	3.0	81.1	162	8	ADX76620	Plant ful	Adx76620	Plant ful	186	29	78.4	224
114	3.0	81.1	204	6	ADA16645	Acinetob	Ada36645	Acinetob	187	29	78.4	224
115	3.0	81.1	341	6	ADB06882	Alloiooc	Abd06882	Alloiooc	188	29	78.4	224
116	3.0	81.1	345	6	ADB06884	Alloiooc	Abd06884	Alloiooc	189	29	78.4	224
117	3.0	81.1	421	7	ABO53138	Klebsiell	Abm53138	Klebsiell	190	29	78.4	224
118	3.0	81.1	437	8	ADX73491	Plant ful	Adx73491	Plant ful	191	29	78.4	224
119	3.0	81.1	528	4	AAG81143	Mycobacte	Aag81143	Mycobacte	192	29	78.4	224
120	3.0	81.1	528	6	ABU34906	Protein e	Abu34906	Protein e	193	29	78.4	224
121	3.0	81.1	528	6	ABU36596	Protein e	Abu36596	Protein e	194	29	78.4	224
122	3.0	81.1	538	7	ABD61131	Baeyer-Vi	Abd61131	Baeyer-Vi	195	29	78.4	224
123	3.0	81.1	553	9	ABE95986	L. pneumo	Abm95986	L. pneumo	196	29	78.4	224
124	3.0	81.1	574	9	AEB81613	L. pneumo	Abm3613	L. pneumo	197	29	78.4	224
125	3.0	81.1	639	4	AAU71928	Human bon	Aau71928	Human bon	198	29	78.4	224
126	3.0	81.1	705	6	ABU49632	Beta-2-mi	Abu49632	Beta-2-mi	199	29	78.4	224
127	3.0	81.1	738	8	ADP29038	C. albica	Adp9038	C. albica	200	29	78.4	224
128	3.0	81.1	1200	3	AAU30768	Baetis ca	Aag30768	Baetis ca	201	29	78.4	224
129	3.0	81.1	1207	3	AGA31076	Arabidops	Agm31076	Arabidops	202	29	78.4	224
130	3.0	81.1	1215	3	AAG310766	Arabidops	Aag310766	Arabidops	203	29	78.4	224
131	3.0	81.1	1526	4	ABB63939	Drosophil	Abb63939	Drosophil	204	29	78.4	224
132	3.0	81.1	29	78.4	AAW25909	Beta-2-mi	Aaw25909	Beta-2-mi	205	29	78.4	224
133	3.0	81.1	29	78.4	AAU25775	Breast ca	Aau25775	Breast ca	206	29	78.4	224
134	3.0	81.1	29	78.4	ABR47819	Human sec	Abm47819	Human sec	207	29	78.4	224
135	3.0	81.1	29	78.4	AGA310767	Human sec	Aag310767	Human sec	208	29	78.4	224
136	3.0	81.1	39	6	ABR0113	Human gen	Abm0113	Human gen	209	29	78.4	224
137	3.0	81.1	39	7	ADB1590	Human sec	Abd1590	Human sec	210	29	78.4	224
138	3.0	81.1	39	7	ADC74205	Human sec	Adc74205	Human sec	211	29	78.4	224
139	3.0	81.1	40	2	AAV07931	Human sec	Aav07931	Human sec	212	29	78.4	224
140	2.9	78.4	40	5	ABP69637	Human pol	Abp69637	Human pol	213	29	78.4	224
141	2.9	78.4	47	5	ABP31160	Human sec	Abp31160	Human sec	214	29	78.4	224
142	2.9	78.4	57	4	ABM0774	Human ova	Abm0774	Human ova	215	29	78.4	224
143	2.9	78.4	77	4	AAM9843	Human exc	Am9843	Human exc	216	29	78.4	224
144	2.9	78.4	77	4	AAM42658	Human kid	Am42658	Human kid	217	29	78.4	224
145	2.9	78.4	81	4	ABG06812	Novel hum	Abg06812	Novel hum	218	29	78.4	224
146	2.9	78.4	99	4	ABG22770	Novel hum	Abg22770	Novel hum	219	29	78.4	224
147	2.9	78.4	111	4	ABG19849	Novel hum	Abg19849	Novel hum	220	29	78.4	224
148	2.9	78.4	124	5	ABP0113	Plant ful	Abp0113	Plant ful	221	29	78.4	224
149	2.9	78.4	134	8	ADY0516	Staphyloc	Ady0516	Staphyloc	222	29	78.4	224
150	2.9	78.4	153	8	ADO1779	Human end	Ado1779	Human end	223	29	78.4	224
151	2.9	78.4	160	4	AAU18472	Human end	Aau18472	Human end	224	29	78.4	224
152	2.9	78.4	162	3	AAB51881	Human sec	Abm51881	Human sec	225	29	78.4	224
153	2.9	78.4	164	3	ABU51880	Gene 2 hu	Abu51880	Gene 2 hu	226	29	78.4	224
154	2.9	78.4	178	4	ADY41709	Human syn	Ady41709	Human syn	227	29	78.4	224
155	2.9	78.4	187	8	ADP9853	Lung spec	Adp9853	Lung spec	228	29	78.4	224
156	2.9	78.4	191	5	ABP39865	Staphyloc	Abp39865	Staphyloc	229	29	78.4	224
157	2.9	78.4	191	8	ADS06905	Staphyloc	Ado6905	Staphyloc	230	29	78.4	224
158	2.9	78.4	204	8	ADM72128	Human NTR	Adm72128	Human NTR	231	29	78.4	224
159	2.9	78.4	224	2	AAW36516	Human syn	Aaw36516	Human syn	232	29	78.4	224
160	2.9	78.4	224	3	ABP44265	Human PRO	Abp44265	Human PRO	233	29	78.4	224
161	2.9	78.4	224	4	ABP24048	Human PRO	Abp24048	Human PRO	234	29	78.4	224
162	2.9	78.4	224	4	AAB64539	Gene 45 h	Abm64539	Gene 45 h	235	29	78.4	224
163	2.9	78.4	224	4	AAB64466	Human sec	Abm64466	Human sec	236	29	78.4	224
164	2.9	78.4	224	4	AAB64540	Human sec	Abm64540	Human sec	237	29	78.4	224
165	2.9	78.4	224	5	ABO25211	Novel hum	Abm25211	Novel hum	238	29	78.4	224
166	2.9	78.4	224	6	ABU72217	Novel hum	Abu72217	Novel hum	239	29	78.4	224
167	2.9	78.4	224	6	ABU84897	Human sec	Abu84897	Human sec	240	29	78.4	224
168	2.9	78.4	224	6	ABU61095	Human PRO	Abu61095	Human PRO	241	29	78.4	224
169	2.9	78.4	224	6	ABU80364	Human sec	Abu80364	Human sec	242	29	78.4	224

ADW17647

ADW17647

ADW17647

ADW17647

ADA24701

ADA24701

ADA24701

ADA24701

Aef64206

Aef64206

Aef64206

Aef64206

Aap9593

Aap9593

Aap9593

Aap9593

Abm45662

Abm45662

Abm45662

Abm45662

Abg02275

Abg02275

Abg02275

Abg02275

Abm4539

Result No.	Score	Query Match Length	DB ID	Description
1	3.3	89.2	371	US-09-5437-68A-4911
2	3.2	86.5	816	Sequence 4911, App
3	3.2	86.5	816	Sequence 3, App
4	3.2	86.5	928	Sequence 3, App
5	3.2	86.5	928	Sequence 1, App
6	3.2	86.5	928	Sequence 8, App
7	3.2	86.5	928	Sequence 5, App
8	3.2	86.5	928	Sequence 4, App
9	3.2	86.5	928	Sequence 4, App
10	3.2	86.5	928	Sequence 8, App
11	3.2	86.5	928	Sequence 4, App
12	3.2	86.5	928	Sequence 3, App
13	3.2	86.5	928	Sequence 8, App
14	3.2	86.5	928	Sequence 2, App
15	3.2	86.5	928	Sequence 3, App
16	3.1	83.8	243	Sequence 16541, App
17	3.1	83.8	324	Sequence 15950, App
18	3.1	83.8	361	Sequence 7933, App
19	3.1	83.8	549	Sequence 28548, App
20	3.0	81.1	204	Sequence 7932, App
21	3.0	81.1	421	Sequence 9655, App
22	3.0	81.1	455	Sequence 16498, App
23	3.0	81.1	528	Sequence 194, App
24	3.0	81.1	681	Sequence 42824, App
25	3.0	81.1	721	Sequence 16497, App
26	2.9	78.4	70	Sequence 4710, App
27	2.9	78.4	151	Sequence 10959, App
28	2.9	78.4	42	Sequence 2, App
29	2.9	78.4	43	Sequence 4638, App
30	2.9	78.4	50	Sequence 18332, App
31	2.9	78.4	51	Sequence 17, App
32	2.9	78.4	52	Sequence 29, App
33	2.9	78.4	53	Sequence 59105, App
34	2.9	78.4	47	Sequence 4, App
35	2.9	78.4	48	Sequence 6, App
36	2.9	78.4	49	Sequence 2, App
37	2.9	78.4	50	Sequence 5, App
38	2.9	78.4	51	Sequence 5, App
39	2.9	78.4	52	Sequence 11319, App
40	2.8	75.7	70	Sequence 10960, App
41	2.8	75.7	71	Sequence 5, App
42	2.8	75.7	72	Sequence 5, App
43	2.8	75.7	73	Sequence 5, App
44	2.8	75.7	74	Sequence 5, App
45	2.8	75.7	75	Sequence 5, App
46	2.8	75.7	76	Sequence 5, App
47	2.8	75.7	77	Sequence 5, App
48	2.8	75.7	78	Sequence 5, App
49	2.8	75.7	79	Sequence 5, App
50	2.8	75.7	80	Sequence 5, App
51	2.8	75.7	81	Sequence 5, App
52	2.8	75.7	82	Sequence 5, App
53	2.8	75.7	83	Sequence 5, App
54	2.8	75.7	84	Sequence 5, App
55	2.8	75.7	85	Sequence 5, App
56	2.8	75.7	86	Sequence 5, App
57	2.8	75.7	87	Sequence 5, App
58	2.8	75.7	88	Sequence 5, App
59	2.8	75.7	89	Sequence 5, App
60	2.8	75.7	90	Sequence 5, App
61	2.8	75.7	91	Sequence 5, App
62	2.8	75.7	92	Sequence 5, App
63	2.8	75.7	93	Sequence 5, App
64	2.8	75.7	94	Sequence 5, App
65	2.8	75.7	95	Sequence 5, App
66	2.8	75.7	96	Sequence 5, App
67	2.8	75.7	97	Sequence 5, App
68	2.8	75.7	98	Sequence 5, App
69	2.8	75.7	99	Sequence 5, App
70	2.8	75.7	100	Sequence 5, App
71	2.8	75.7	101	Sequence 5, App
72	2.8	75.7	102	Sequence 5, App
73	2.8	75.7	103	Sequence 5, App
74	2.8	75.7	104	Sequence 5, App
75	2.8	75.7	105	Sequence 5, App
76	2.8	75.7	106	Sequence 5, App
77	2.8	75.7	107	Sequence 5, App
78	2.8	75.7	108	Sequence 5, App
79	2.8	75.7	109	Sequence 5, App
80	2.8	75.7	110	Sequence 5, App
81	2.8	75.7	111	Sequence 5, App
82	2.8	75.7	112	Sequence 5, App
83	2.8	75.7	113	Sequence 5, App
84	2.8	75.7	114	Sequence 5, App
85	2.8	75.7	115	Sequence 5, App
86	2.8	75.7	116	Sequence 5, App
87	2.8	75.7	117	Sequence 5, App
88	2.8	75.7	118	Sequence 5, App
89	2.8	75.7	119	Sequence 5, App
90	2.8	75.7	120	Sequence 5, App
91	2.8	75.7	121	Sequence 5, App
92	2.8	75.7	122	Sequence 5, App
93	2.8	75.7	123	Sequence 5, App
94	2.8	75.7	124	Sequence 5, App
95	2.8	75.7	125	Sequence 5, App
96	2.8	75.7	126	Sequence 5, App
97	2.8	75.7	127	Sequence 5, App
98	2.8	75.7	128	Sequence 5, App
99	2.8	75.7	129	Sequence 5, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query Match Length	DB ID	Description
1	3.3	89.2	371	US-09-5437-68A-4911
2	3.2	86.5	816	Sequence 4911, App
3	3.2	86.5	816	Sequence 3, App
4	3.2	86.5	928	Sequence 1, App
5	3.2	86.5	928	Sequence 8, App
6	3.2	86.5	928	Sequence 5, App
7	3.2	86.5	928	Sequence 4, App
8	3.2	86.5	928	Sequence 4, App
9	3.2	86.5	928	Sequence 8, App
10	3.2	86.5	928	Sequence 4, App
11	3.2	86.5	928	Sequence 3, App
12	3.2	86.5	928	Sequence 8, App
13	3.2	86.5	928	Sequence 2, App
14	3.2	86.5	928	Sequence 3, App
15	3.2	86.5	928	Sequence 16541, App
16	3.1	83.8	243	Sequence 15950, App
17	3.1	83.8	324	Sequence 7933, App
18	3.1	83.8	361	Sequence 28548, App
19	3.1	83.8	549	Sequence 7932, App
20	3.0	81.1	204	Sequence 9655, App
21	3.0	81.1	421	Sequence 16498, App
22	3.0	81.1	455	Sequence 194, App
23	3.0	81.1	528	Sequence 42824, App
24	3.0	81.1	681	Sequence 16497, App
25	3.0	81.1	721	Sequence 4710, App
26	2.9	78.4	70	Sequence 49066, App

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OM protein - protein search, using BW mode.

Run on: October 13, 2006, 01:05:12 (without alignments)

11.783 Million cell updates/sec

Title: US-10-537-648-1  
Perfect score: 37  
Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62  
Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591  
Listing first 1000 summaries

Database : Issued Patents AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaas/5\_COMB.dep:  
2: /BMC\_Celerra\_SIDS3/ptodata/2/iaas/6\_COMB.dep:  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaas/7\_COMB.dep:  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaas/H\_COMB.dep:  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaas/IPTUS\_COMB.dep:  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaas/IRE\_COMB.dep:  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaas/baChffiles1.pop:\*

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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101	27	73.0	168	2	US-09-602-797A-88	Sequence 88, APP1	Sequence 11, APP1
102	27	73.0	173	2	US-09-249-799A-1745	Sequence 17745, A	Sequence 11, APP1
103	27	73.0	180	2	US-09-270-767-44336	Sequence 44236, A	Sequence 7061, APP1
104	27	73.0	220	2	US-09-252-991A-24796	Sequence 24796, A	Sequence 9285, APP1
105	27	73.0	233	2	US-09-302-540-14404	Sequence 14404, A	Sequence 16, APP1
106	27	73.0	243	2	US-09-270-767-33470	Sequence 33470, A	Sequence 16, APP1
107	27	73.0	243	2	US-09-270-767-48687	Sequence 48687, A	Sequence 46, APP1
108	27	73.0	283	2	US-09-252-991A-20071	Sequence 20071, A	Sequence 3814, APP1
109	27	73.0	348	2	US-09-495-880A-13	Sequence 13, APP1	Sequence 4765, APP1
110	27	73.0	348	2	US-09-495-880A-33	Sequence 28, APP1	Sequence 2, APP1
111	27	73.0	348	2	US-09-495-880A-33	Sequence 33, APP1	Sequence 92, APP1
112	27	73.0	358	2	US-09-107-53A-4143	Sequence 4143, APP1	Sequence 42532, A
113	27	73.0	358	2	US-09-248-79A-22778	Sequence 22578, A	Sequence 92, APP1
114	27	73.0	421	2	US-09-198-452A-535	Sequence 535, APP1	Sequence 22990, A
115	27	73.0	503	2	US-09-248-79A-16512	Sequence 16512, A	Sequence 10944, A
116	27	73.0	525	2	US-09-328-79A-497	Sequence 497, APP1	Sequence 13886, APP1
117	27	73.0	536	2	US-09-107-431-2945	Sequence 24548, A	Sequence 3, APP1
118	27	73.0	602	2	US-09-248-79A-24348	Sequence 84, APP1	Sequence 2, APP1
119	27	73.0	613	2	US-09-602-77A-84	Sequence 18862, A	Sequence 6, APP1
120	27	73.0	503	2	US-09-583-110-4277	Sequence 4277, APP1	Sequence 6, APP1
121	27	73.0	503	2	US-09-769-787-74	Sequence 74, APP1	Sequence 6, APP1
122	27	73.0	525	2	US-09-328-532-7767	Sequence 767, APP1	Sequence 18617, A
123	27	73.0	536	2	US-09-107-431-2945	Sequence 2945, APP1	Sequence 7567, APP1
124	27	73.0	602	2	US-09-248-79A-20114	Sequence 20214, A	Sequence 33199, A
125	27	73.0	613	2	US-09-248-79A-14110	Sequence 14110, A	Sequence 48415, A
126	27	73.0	754	2	US-09-270-767-42479	Sequence 42479, A	Sequence 58387, A
127	27	73.0	761	3	US-10-114-270-108	Sequence 108, APP1	Sequence 996, APP1
128	27	73.0	881	2	US-09-489-039A-12003	Sequence 12003, A	Sequence 82, APP1
129	27	73.0	881	2	US-09-489-039A-12003	Sequence 1370, APP1	Sequence 84, APP1
130	27	73.0	937	2	US-09-543-68A-5513	Sequence 5513, APP1	Sequence 2, APP1
131	27	73.0	2441	1	US-08-194-468-2	Sequence 2, APP1	Sequence 2, APP1
132	27	73.0	2441	1	US-08-961-739-2	Sequence 2, APP1	Sequence 2, APP1
133	27	73.0	2441	2	US-09-514-242A-8	Sequence 8, APP1	Sequence 2, APP1
134	27	73.0	2442	2	US-09-686-311-2	Sequence 10, APP1	Sequence 2, APP1
135	27	73.0	2442	2	US-09-514-242A-10	Sequence 10, APP1	Sequence 2, APP1
136	27	73.0	2442	2	US-09-518-092-1370	Sequence 1370, APP1	Sequence 2, APP1
137	27	73.0	3672	1	US-08-194-445-12	Sequence 12, APP1	Sequence 2, APP1
138	27	73.0	3672	2	US-09-396-540-12	Sequence 12, APP1	Sequence 2, APP1
139	27	73.0	3801	1	US-09-822-445-10	Sequence 10, APP1	Sequence 2, APP1
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141	26	70.3	62	2	US-09-102-626B-32	Sequence 32, APP1	Sequence 27, APP1
142	26	70.3	68	2	US-09-621-976-6132	Sequence 6132, APP1	Sequence 27, APP1
143	26	70.3	86	2	US-09-312-626B-34	Sequence 34, APP1	Sequence 27, APP1
144	26	70.3	88	2	US-09-543-68A-8203	Sequence 8203, APP1	Sequence 27, APP1
145	26	70.3	103	2	US-09-543-68A-5144	Sequence 5444, APP1	Sequence 33, APP1
146	26	70.3	124	2	US-09-640-211A-2157	Sequence 2157, APP1	Sequence 4, APP1
147	26	70.3	135	2	US-10-190-902B-5	Sequence 5, APP1	Sequence 9617, APP1
148	26	70.3	146	2	US-10-104-047-2422	Sequence 2422, APP1	Sequence 21491, APP1
149	26	70.3	162	2	US-09-439-039A-7276	Sequence 7276, APP1	Sequence 9, APP1
150	26	70.3	184	2	US-09-489-039A-9527	Sequence 9522, APP1	Sequence 8, APP1
151	26	70.3	185	2	US-09-114-000C-6497	Sequence 6497, APP1	Sequence 7166, APP1
152	26	70.3	190	2	US-08-88-207A-505	Sequence 505, APP1	Sequence 14859, APP1
153	26	70.3	209	2	US-09-134-000C-5222	Sequence 5232, APP1	Sequence 15920, APP1
154	26	70.3	220	2	US-09-198-452A-461	Sequence 461, APP1	Sequence 15777, APP1
155	26	70.3	220	2	US-09-210-767-33951	Sequence 33951, APP1	Sequence 18625, APP1
156	26	70.3	220	2	US-09-210-767-49168	Sequence 49168, APP1	Sequence 2555, APP1
157	26	70.3	220	2	US-09-418-186A-442	Sequence 442, APP1	Sequence 673, APP1
158	26	70.3	225	2	US-09-902-540-15556	Sequence 15456, A	Sequence 20159, APP1
159	26	70.3	228	2	US-09-902-540-14499	Sequence 14499, A	Sequence 20278, APP1
160	26	70.3	235	2	US-10-094-749-2324	Sequence 2324, APP1	Sequence 29, APP1
161	26	70.3	238	2	US-09-489-039A-10312	Sequence 10132, APP1	Sequence 2, APP1
162	26	70.3	239	2	US-09-210-767-49168	Sequence 25501, APP1	Sequence 23318, APP1
163	26	70.3	252	2	US-09-543-681A-6220	Sequence 6220, APP1	Sequence 20159, APP1
164	26	70.3	256	2	US-09-210-767-33129	Sequence 33129, A	Sequence 20278, APP1
165	26	70.3	265	2	US-09-210-767-48346	Sequence 48346, A	Sequence 29, APP1
166	26	70.3	265	2	US-09-328-352-6989	Sequence 6989, APP1	Sequence 2, APP1
167	26	70.3	279	2	US-09-248-79A-18625	Sequence 2661, APP1	Sequence 26, APP1
168	26	70.3	280	2	US-10-212-4490-86	Sequence 86, APP1	Sequence 14, APP1
169	26	70.3	280	2	US-09-540-243-2476	Sequence 2476, APP1	Sequence 6791, APP1
170	26	70.3	296	2	US-09-724-623-103	Sequence 103, APP1	Sequence 10445, APP1
172	26	70.3	296	3	US-10-288-930-103	Sequence 103,	Sequence 10445, APP1

Result No.	Score	Query	Match	Length	DB	ID	Description
1	7	100.0	7	6	US-10-537-648-1	Sequence 40368, A	Sequence 1, Appli
2	5	71.4	117	7	US-11-310-403-12870	Sequence 12870, A	Sequence 2, Appli
3	5	71.4	135	6	US-10-953-349-8189	Sequence 8189, AP	Sequence 3, Appli
4	5	71.4	177	6	US-10-953-349-2799	Sequence 2799, AP	Sequence 4, Appli
5	5	71.4	202	6	US-10-953-349-2798	Sequence 2798, AP	Sequence 5, Appli
6	5	71.4	293	6	US-10-526-572-17	Sequence 17, APPI	Sequence 6, Appli
7	5	71.4	303	6	US-10-449-902-30928	Sequence 30928, A	Sequence 7, APPI
8	5	71.4	303	6	US-10-734-719-29	Sequence 29, APPI	Sequence 8, APPI
9	5	71.4	334	7	US-11-330-403-7912	Sequence 7912, APPI	Sequence 9, APPI
10	5	71.4	384	6	US-10-449-902-40368	Sequence 40368, A	Sequence 10, APPI
11	5	71.4	397	7	US-11-310-403-3473	Sequence 3473, AP	Sequence 11, APPI
12	5	71.4	399	6	US-10-449-902-43766	Sequence 43766, A	Sequence 12, APPI
13	5	71.4	403	6	US-10-953-349-3753	Sequence 3753, AP	Sequence 13, APPI
14	5	71.4	406	6	US-10-953-349-3752	Sequence 3752, AP	Sequence 14, APPI
15	5	71.4	407	6	US-10-449-902-28693	Sequence 28693, A	Sequence 15, APPI
16	5	71.4	421	7	US-11-310-403-14843	Sequence 14843, A	Sequence 16, APPI
17	6	71.4	422	6	US-10-953-349-3751	Sequence 3751, AP	Sequence 17, APPI
18	5	71.4	472	6	US-10-669-902-1418	Sequence 1418, AP	Sequence 18, APPI
19	5	71.4	493	6	US-10-953-349-18397	Sequence 18397, A	Sequence 19, APPI
20	5	71.4	563	6	US-10-449-902-43710	Sequence 43710, A	Sequence 20, APPI
21	5	71.4	563	6	US-10-449-902-53474	Sequence 53474, A	Sequence 21, APPI
22	5	71.4	594	6	US-10-449-902-52050	Sequence 52090, A	Sequence 22, APPI
23	5	71.4	595	6	US-10-449-902-38085	Sequence 38085, A	Sequence 23, APPI
24	5	71.4	619	6	US-10-449-902-56241	Sequence 56241, A	Sequence 24, APPI
25	5	71.4	694	6	US-10-539-228-313	Sequence 313, APPI	Sequence 25, APPI

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	7	100.0	7	6	US-10-537-648-1	Sequence 40368, A	Sequence 1, Appli
2	5	71.4	117	7	US-11-310-403-12870	Sequence 12870, A	Sequence 2, Appli
3	5	71.4	135	6	US-10-953-349-8189	Sequence 8189, AP	Sequence 3, Appli
4	5	71.4	177	6	US-10-953-349-2799	Sequence 2799, AP	Sequence 4, Appli
5	5	71.4	202	6	US-10-953-349-2798	Sequence 2798, AP	Sequence 5, Appli
6	5	71.4	293	6	US-10-526-572-17	Sequence 17, APPI	Sequence 6, APPI
7	5	71.4	303	6	US-10-449-902-30928	Sequence 30928, A	Sequence 7, APPI
8	5	71.4	303	6	US-10-734-719-29	Sequence 29, APPI	Sequence 8, APPI
9	5	71.4	334	7	US-11-330-403-7912	Sequence 7912, APPI	Sequence 9, APPI
10	5	71.4	384	6	US-10-449-902-40368	Sequence 40368, A	Sequence 10, APPI
11	5	71.4	397	7	US-11-310-403-3473	Sequence 3473, AP	Sequence 11, APPI
12	5	71.4	399	6	US-10-449-902-43766	Sequence 43766, A	Sequence 12, APPI
13	5	71.4	403	6	US-10-953-349-3753	Sequence 3753, AP	Sequence 13, APPI
14	5	71.4	406	6	US-10-953-349-3752	Sequence 3752, AP	Sequence 14, APPI
15	5	71.4	407	6	US-10-449-902-28693	Sequence 28693, A	Sequence 15, APPI
16	5	71.4	421	7	US-11-310-403-14843	Sequence 14843, A	Sequence 16, APPI
17	6	71.4	422	6	US-10-953-349-3751	Sequence 3751, AP	Sequence 17, APPI
18	5	71.4	472	6	US-10-669-902-1418	Sequence 1418, AP	Sequence 18, APPI
19	5	71.4	493	6	US-10-953-349-18397	Sequence 18397, A	Sequence 19, APPI
20	5	71.4	563	6	US-10-449-902-43710	Sequence 43710, A	Sequence 20, APPI
21	5	71.4	563	6	US-10-449-902-53474	Sequence 53474, A	Sequence 21, APPI
22	5	71.4	594	6	US-10-449-902-52050	Sequence 52090, A	Sequence 22, APPI
23	5	71.4	595	6	US-10-449-902-38085	Sequence 38085, A	Sequence 23, APPI
24	5	71.4	619	6	US-10-449-902-56241	Sequence 56241, A	Sequence 24, APPI
25	5	71.4	694	6	US-10-539-228-313	Sequence 313, APPI	Sequence 25, APPI

99	7	US-11-229-770-545	Sequence 53, App
100	4	US-11-043-842-586	Sequence 66, App
101	4	US-11-265-762-132	Sequence 68, App
102	4	US-10-953-349-11948	Sequence 8, App
103	4	US-10-953-349-14117	Sequence 16, App
104	4	US-11-229-770-1160	Sequence 44, App
105	4	US-11-043-349-4116	Sequence 48, App
106	4	US-10-539-228-760	Sequence 52, App
107	4	US-10-953-349-11947	Sequence 56, App
108	4	US-10-953-349-13901	Sequence 60, App
109	4	US-11-056-35494	Sequence 64, App
110	4	US-11-056-355B-58204	Sequence 68, App
111	4	US-10-449-902-56313	Sequence 72, App
112	4	US-11-043-842-191	Sequence 76, App
113	4	US-10-953-613C-1010	Sequence 80, App
114	4	US-11-091-234A-30	Sequence 84, App
115	4	US-10-953-613C-1005	Sequence 88, App
116	4	US-11-091-234A-25	Sequence 92, App
117	4	US-10-953-613C-1009	Sequence 96, App
118	4	US-11-091-234A-29	Sequence 100, App
119	4	US-10-953-613C-1000	Sequence 104, App
120	4	US-11-091-234A-20	Sequence 108, App
121	4	US-11-434-137-7284	Sequence 112, App
122	4	US-11-091-234A-25	Sequence 116, App
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132	4	US-11-330-403-7865	Sequence 156, App
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140	4	US-11-434-137-10585	Sequence 188, App
141	4	US-11-091-234A-21	Sequence 192, App
142	4	US-10-953-613C-997	Sequence 196, App
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193	4	US-11-249-296-16	Sequence 400, App
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336	4	US-11-154-103-58	Sequence 972, App
337	4	US-11-154-103-58	Sequence 976, App
338	4	US-11-154-103-58	Sequence 980, App
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2	5	71.4	70	2	US-09-489/539A-13139	Sequence 13139, A	Sequence 13139, A
3	5	71.4	135	2	US-10-190/502B-5	Sequence 5, AP	Sequence 5, AP
4	5	71.4	146	2	US-10-104-047-2422	Sequence 2422, AP	Sequence 2422, AP
5	5	71.4	151	2	US-09-105-703B-2140	Sequence 2140, AP	Sequence 2140, AP
6	5	71.4	160	2	US-09-270-167-33849	Sequence 4906, A	Sequence 4906, A
7	5	71.4	161	2	US-09-248-196A-16520	Sequence 33849, A	Sequence 33849, A
8	5	71.4	163	2	US-09-134-001C-4710	Sequence 16500, A	Sequence 16500, A
9	5	71.4	191	2	US-09-134-001C-4710	Sequence 4710, AP	Sequence 4710, AP
10	5	71.4	191	2	US-09-134-001C-4710	Sequence 393, AP	Sequence 393, AP
11	5	71.4	224	1	US-08-700-537-2	Sequence 2, AP	Sequence 2, AP
12	5	71.4	224	2	US-09-199-833A-162	Sequence 162, AP	Sequence 162, AP
13	5	71.4	224	2	US-10-020-145A-162	Sequence 162, AP	Sequence 162, AP
14	5	71.4	224	2	US-09-978-189-162	Sequence 162, AP	Sequence 162, AP
15	5	71.4	224	2	US-10-017-055A-162	Sequence 162, AP	Sequence 162, AP
16	5	71.4	224	3	US-10-145-129A-162	Sequence 162, AP	Sequence 162, AP
17	5	71.4	224	3	US-10-013-329A-162	Sequence 162, AP	Sequence 162, AP
18	5	71.4	224	3	US-10-013-911A-162	Sequence 162, AP	Sequence 162, AP
19	5	71.4	225	2	US-09-002-540-15456	Sequence 15456, A	Sequence 15456, A
20	5	71.4	233	2	US-09-902-040-14404	Sequence 14404, A	Sequence 14404, A
21	5	71.4	254	2	US-09-449-437A-4	Sequence 4, AP	Sequence 4, AP
22	5	71.4	254	3	US-09-149-437A-6	Sequence 6, AP	Sequence 6, AP
23	5	71.4	254	2	US-09-195-106-2	Sequence 2, AP	Sequence 2, AP
24	5	71.4	258	2	US-09-152-6909	Sequence 6988, AP	Sequence 6988, AP
25	5	71.4	263	2	US-09-134-001C-4638	Sequence 4638, AP	Sequence 4638, AP
26	5	71.4	280	2	US-10-272-490-86	Sequence 86, AP	Sequence 86, AP

100	5	71.4	928	2	US-09-758-007-3	Sequence 3, Appli	173	1	US-08-237-418-5	Sequence 5, Appli
101	5	71.4	928	2	US-10-441-510-8	Sequence 8, Appli	174	4	US-09-168-312-5	Sequence 2, Appli
102	5	71.4	928	5	PCT-US94-10357-2	Sequence 2, Appli	175	4	US-09-578-318-5	Sequence 5, Appli
103	5	71.4	928	5	PCT-US94-10357-3	Sequence 3, Appli	176	4	US-10-340-783-5	Sequence 5, Appli
104	5	71.4	978	2	US-09-949-016-8098	Sequence 8098, Appli	177	4	US-09-902-540-14233	Sequence 1,2,3, A
105	5	71.4	986	2	US-09-248-796A-19088	Sequence 19088, Appli	178	4	US-09-557-771-34	Sequence 34, Appli
106	5	71.4	1046	2	US-09-199-637A-13	Sequence 13, Appli	179	4	US-10-340-650-34	Sequence 34, Appli
107	5	71.4	1196	2	US-09-275-252A-9	Sequence 9, Appli	180	4	US-10-340-650-34	Sequence 34, Appli
108	5	71.4	1233	2	US-09-328-352-5704	Sequence 5104, Appli	181	4	US-10-340-650-34	Sequence 34, Appli
109	5	71.4	1236	2	US-09-176-644-21	Sequence 21, Appli	182	4	US-10-340-583-34	Sequence 34, Appli
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111	5	71.4	1262	2	US-09-176-644-22	Sequence 22, Appli	184	4	US-10-340-582-34	Sequence 34, Appli
112	5	71.4	1262	2	US-09-519-076-22	Sequence 22, Appli	185	4	US-10-340-653A-34	Sequence 34, Appli
113	5	71.4	1262	2	US-09-328-352-5704	Sequence 5104, Appli	186	4	US-09-270-767-5462	Sequence 34, Appli
114	5	71.4	1342	2	US-09-561-709B-13	Sequence 13, Appli	187	4	US-09-270-767-5462	Sequence 34, Appli
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116	5	71.4	1504	2	US-09-352-7046	Sequence 7046, Appli	189	4	US-08-168-850A-27	Sequence 27, Appli
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121	4	57.1	7	2	US-09-020-065A-7	Sequence 7, Appli	194	4	US-08-911-982-37	Sequence 37, Appli
122	4	57.1	7	2	US-10-834-424-35	Sequence 35, Appli	195	4	US-08-911-982-38	Sequence 38, Appli
123	4	57.1	8	2	US-09-020-065A-24	Sequence 24, Appli	196	4	US-08-369-241-148	Sequence 1,4,8, App
124	4	57.1	8	2	US-09-715-763A-10	Sequence 10, Appli	197	4	US-10-062-548-148	Sequence 1,4,8, App
125	4	57.1	8	2	US-09-715-763A-12	Sequence 12, Appli	198	4	US-09-270-767-5986	Sequence 5,8,6,6, A
126	4	57.1	9	1	US-09-765-179B-17	Sequence 17, Appli	199	4	US-09-369-247-134	Sequence 13,4, A
127	4	57.1	9	2	US-09-641-709B-11	Sequence 21,8, Appli	200	4	US-09-332-210-923	Sequence 9,23, App
128	4	57.1	9	3	US-09-641-528B-31508	Sequence 8, Appli	201	4	US-10-062-548-134	Sequence 1,4,8, App
129	4	57.1	10	2	US-08-973-551-8	Sequence 8, Appli	202	4	US-09-513-999C-5758	Sequence 75,8, App
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133	4	57.1	11	1	US-08-306-546C-25	Sequence 25, Appli	206	4	US-09-621-972-4391	Sequence 4,3,1, AP
134	4	57.1	11	1	US-08-530-524A-25	Sequence 25, Appli	207	4	US-10-340-783-6	Sequence 6, Appli
135	4	57.1	11	3	US-09-641-528B-1990	Sequence 1990, Appli	208	4	US-09-205-528-545	Sequence 5,5,5, App
136	4	57.1	11	3	US-09-641-528B-24394	Sequence 24394, Appli	209	4	US-09-513-999C-6296	Sequence 6,2,6, AP
137	4	57.1	11	3	US-09-641-528B-31410	Sequence 31410, Appli	210	4	US-10-004-860-545	Sequence 5,4,5, App
138	4	57.1	11	3	US-09-641-528B-31669	Sequence 31669, Appli	211	4	US-09-004-860-6	Sequence 6, Appli
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141	4	57.1	12	2	US-08-434-831B-21	Sequence 21, Appli	214	4	US-09-270-767-53216	Sequence 5,3,2,16, A
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143	4	57.1	13	2	US-08-505-250-7	Sequence 7, Appli	216	4	US-09-202-548B-1	Sequence 19,23, AP
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145	4	57.1	15	2	US-09-053-611-38	Sequence 38, Appli	218	4	US-09-72-634-10	Sequence 1, Appi
146	4	57.1	15	2	US-09-526-195-5	Sequence 5, Appli	219	4	US-09-716-129-64	Sequence 6,4,6, AP
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148	4	57.1	15	3	US-09-641-528B-46385	Sequence 46185, Appli	221	4	US-09-513-999C-6957	Sequence 6,9,7, AP
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150	4	57.1	15	3	US-08-480-473B-21	Sequence 21, Appli	223	4	US-09-312-626B-32	Sequence 31,906, A
151	4	57.1	18	2	US-08-915-213-21	Sequence 21, Appli	224	4	US-09-912-858-1	Sequence 1, Appi
152	4	57.1	18	2	US-09-235-217-21	Sequence 21, Appli	225	4	US-09-134-000C-6046	Sequence 6,46, AP
153	4	57.1	18	3	US-09-991-797A-2	Sequence 2, Appli	226	4	US-09-583-110-3460	Sequence 3,4,6,0, AP
154	4	57.1	18	5	PCT-US96-0251-21	Sequence 21, Appli	227	4	US-09-248-796A-24729	Sequence 21,2,9, AP
155	4	57.1	19	1	US-09-149-476-675	Sequence 675, Appli	228	4	US-09-513-999C-4960	Sequence 4,9,6,0, AP
156	4	57.1	19	1	US-08-480-473B-21	Sequence 21, Appli	229	4	US-09-252-99A-31906	Sequence 1,1,60, AP
157	4	57.1	20	1	US-08-914-915-89	Sequence 89, Appli	230	4	US-09-912-858-23	Sequence 1,1,60, AP
158	4	57.1	20	2	US-09-623-548A-102	Sequence 118, Appli	231	4	US-09-270-767-59376	Sequence 5,9,76, A
159	4	57.1	20	2	US-09-657-276-302	Sequence 302, Appli	232	4	US-09-583-110-5069	Sequence 5,069, AP
160	4	57.1	21	2	US-09-563-222C-98	Sequence 98, Appli	233	4	US-09-107-433-4759	Sequence 4,7,59, AP
161	4	57.1	21	2	US-09-563-222C-101	Sequence 101, Appli	234	4	US-09-248-796A-24750	Sequence 4,9,6,0, AP
162	4	57.1	22	1	US-07-988-925-12	Sequence 12, Appli	235	4	US-09-205-258-1160	Sequence 1,1,60, AP
163	4	57.1	22	1	US-08-362-780-12	Sequence 12, Appli	236	4	US-10-004-860-1160	Sequence 1,1,60, AP
164	4	57.1	22	2	US-09-528-118	Sequence 118, Appli	237	4	US-09-270-767-59376	Sequence 5,9,76, A
165	4	57.1	22	2	US-09-563-222C-87	Sequence 87, Appli	238	4	US-09-583-110-5069	Sequence 5,069, AP
166	4	57.1	22	2	US-09-563-222C-91	Sequence 91, Appli	239	4	US-09-107-433-4759	Sequence 4,7,59, AP
167	4	57.1	22	2	US-09-563-222C-95	Sequence 95, Appli	240	4	US-09-248-796A-24750	Sequence 4,9,6,0, AP
168	4	57.1	22	2	US-09-563-222C-105	Sequence 105, Appli	241	4	US-09-513-999C-4967	Sequence 4,9,7, AP
169	4	57.1	22	2	US-08-478-684G-12	Sequence 12, Appli	242	4	US-09-248-796A-24750	Sequence 4,9,52, A
170	4	57.1	28	2	US-09-471-276-819	Sequence 819, Appli	243	4	US-09-248-796A-24750	Sequence 4,9,53, A
171	4	57.1	28	2	US-10-001-887-123	Sequence 123, Appli	244	4	US-09-107-433-4759	Sequence 4,7,59, AP
172	4	57.1	32	2	US-09-242-890-5	Sequence 5, Appli	245	4	US-09-149-476-543	Sequence 5,43, AP

Result No.	Score	Query	Match	Length	DB	ID	Description
1	6	85.7	290	2	A82236		pseudouridine synth
2	6	85.7	1375	2	T13822		frazzled gene prot
3	6	85.7	1526	2	T13823		frazzled gene prot
4	5	71.4	93	2	AF2246		hypothetical prote
5	5	71.4	135	2	G84469		probable glycine-r
6	5	71.4	157	2	T46440		hypothetical prote
7	5	71.4	177	2	G96794		probable calmoduli
8	5	71.4	193	2	T06972		hypothetical prote
9	5	71.4	206	2	H64023		hypothetical prote
10	5	71.4	214	2	S21169		19K zein precursor
11	5	71.4	220	2	S01838		nify protein - Kle
12	5	71.4	228	2	T42057		hypothetical prote
13	5	71.4	229	2	D81667		conserved hypothet
14	5	71.4	229	2	H81073		conserved hypothet
15	5	71.4	234	2	Z12ZM3		19K zein precursor
16	5	71.4	234	2	S27643		19K zein precursor
17	5	71.4	234	2	S03417		hypothetical prote
18	5	71.4	234	2	T20603		lectin II - Scotch
19	5	71.4	249	2	JQ1381		hypothetical prote
20	5	71.4	253	2	T49820		conserved hypothet
21	5	71.4	258	2	H75436		homoeotic protein s
22	5	71.4	284	2	D70080		transcription regul
23	5	71.4	291	2	A40587		probable transcript
24	5	71.4	295	2	T52117		zinc finger protei
25	5	71.4	298	2	F81118		probable galactosy
26	5	71.4	303	2	T34112		hypothetical prote
27	5	71.4	310	2	E90167		hypothetical prote
28	5	71.4	310	2	D85751		hypothetical prote
29	5	71.4	310	2	PL0189		hypothetical prote

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	6	85.7	290	2	A82236		pseudouridine synt
2	6	85.7	1375	2	T13822		frazzled gene prot
3	6	85.7	1526	2	T13823		frazzled gene prot
4	5	71.4	93	2	AF2246		hypothetical prote
5	5	71.4	135	2	G84469		probable glycine-r
6	5	71.4	157	2	T46440		hypothetical prote
7	5	71.4	177	2	G96794		probable calmoduli
8	5	71.4	193	2	T06972		hypothetical prote
9	5	71.4	206	2	H64023		hypothetical prote
10	5	71.4	214	2	S21169		19K zein precursor
11	5	71.4	220	2	S01838		19K zein precursor
12	5	71.4	228	2	T42057		hypothetical prote
13	5	71.4	229	2	D81667		conserved hypothet
14	5	71.4	229	2	H81073		conserved hypothet
15	5	71.4	234	2	Z12ZM3		19K zein precursor
16	5	71.4	234	2	S27643		19K zein precursor
17	5	71.4	234	2	S03417		hypothetical prote
18	5	71.4	234	2	T20603		lectin II - Scotch
19	5	71.4	249	2	JQ1381		hypothetical prote
20	5	71.4	253	2	T49820		conserved hypothet
21	5	71.4	258	2	H75436		homoeotic protein s
22	5	71.4	284	2	D70080		transcription regul
23	5	71.4	291	2	A40587		probable transcript
24	5	71.4	295	2	T52117		zinc finger protei
25	5	71.4	298	2	F81118		probable galactosy
26	5	71.4	303	2	T34112		hypothetical prote
27	5	71.4	310	2	E90167		hypothetical prote
28	5	71.4	310	2	D85751		hypothetical prote
29	5	71.4	310	2	PL0189		hypothetical prote

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

103	4	57.1	30	2	S70341	176	4	57.1	100	2	E85677
104	4	57.1	31	2	S77593	177	4	57.1	100	2	A99818
105	4	57.1	36	2	C37473	178	4	57.1	100	2	D87057
106	4	57.1	49	2	E86636	179	4	57.1	101	2	S10387
107	4	57.1	49	2	G82678	180	4	57.1	101	2	B47624
108	4	57.1	51	2	AB0546	181	4	57.1	101	2	B39075
109	4	57.1	54	2	AH1885	182	4	57.1	103	1	L1HONM
110	4	57.1	57	2	A49111	183	4	57.1	103	2	S08462
111	4	57.1	61	1	DNPBPF	184	4	57.1	103	2	360677
112	4	57.1	61	2	C82536	185	4	57.1	104	2	T04149
113	4	57.1	62	2	AD2912	186	4	57.1	104	2	S36064
114	4	57.1	64	2	T25247	187	4	57.1	105	2	S44124
115	4	57.1	64	2	B97177	188	4	57.1	105	2	S52680
116	4	57.1	64	2	H98033	189	4	57.1	106	1	I. LAHUKN
117	4	57.1	64	2	H98046	190	4	57.1	106	1	I. LAHUKN
118	4	57.1	67	2	F81853	191	4	57.1	106	1	I. LAHOML
119	4	57.1	69	2	JH0348	192	4	57.1	106	1	I. LAHDX
120	4	57.1	70	2	PC2063	193	4	57.1	107	1	I. LAHUL
121	4	57.1	70	2	AH2112	194	4	57.1	107	2	B46516
122	4	57.1	72	1	Q38072	195	4	57.1	107	2	TJH0347
123	4	57.1	72	2	D85557	196	4	57.1	107	2	A82653
124	4	57.1	72	2	T12404	197	4	57.1	108	2	A12341
125	4	57.1	72	2	T11887	198	4	57.1	108	2	JN0695
126	4	57.1	73	2	A10290	199	4	57.1	109	1	L1HUEP
127	4	57.1	73	2	AH2157	200	4	57.1	109	1	L1HUNA
128	4	57.1	75	1	AB2497	201	4	57.1	109	2	L2HUBR
129	4	57.1	76	1	W5M158	202	4	57.1	109	2	S68171
130	4	57.1	76	2	T45556	203	4	57.1	110	1	L2HUS8
131	4	57.1	77	2	IQ1295	204	4	57.1	110	2	S36258
132	4	57.1	78	2	B90778	205	4	57.1	110	2	S57428
133	4	57.1	78	2	D70001	206	4	57.1	110	2	S57412
134	4	57.1	78	2	AH2386	207	4	57.1	110	2	S57408
135	4	57.1	80	2	F81467	208	4	57.1	110	2	S57442
136	4	57.1	80	2	AB2345	209	4	57.1	110	2	S51149
137	4	57.1	80	2	T45556	210	4	57.1	110	2	F84670
138	4	57.1	81	2	150975	211	4	57.1	110	2	G72597
139	4	57.1	81	2	151144	212	4	57.1	111	1	L1HDNG
140	4	57.1	81	2	151145	213	4	57.1	111	1	L1HUNW
141	4	57.1	81	2	DB81940	214	4	57.1	111	1	L1HUV0
142	4	57.1	85	2	AF1548	215	4	57.1	111	1	L2HUBH
143	4	57.1	86	2	B81144	216	4	57.1	111	1	L2HUBO
144	4	57.1	86	2	S11229	217	4	57.1	111	1	L2HUMC
145	4	57.1	87	2	AD3551	218	4	57.1	111	1	L2HUND
146	4	57.1	87	2	W9Y2RF	219	4	57.1	111	1	L2HUTG
147	4	57.1	89	2	E98123	220	4	57.1	111	1	L2HUTR
148	4	57.1	89	2	AG3194	221	4	57.1	111	1	L2HUVL
149	4	57.1	90	2	C83960	222	4	57.1	111	1	L2HUNW
150	4	57.1	91	2	C90867	223	4	57.1	111	2	L6HULD
151	4	57.1	91	2	AG2691	224	4	57.1	111	2	L6HUST
152	4	57.1	92	2	C97473	225	4	57.1	111	1	L1HOMT
153	4	57.1	93	2	D61039	226	4	57.1	111	2	S46396
154	4	57.1	94	2	AC3130	227	4	57.1	111	2	S19671
155	4	57.1	94	2	S72964	228	4	57.1	111	2	S47185
156	4	57.1	95	2	S73920	229	4	57.1	111	2	S38499
157	4	57.1	96	2	S3065	230	4	57.1	111	2	S47009
158	4	57.1	97	2	S76170	231	4	57.1	111	2	S36256
159	4	57.1	97	2	E53174	232	4	57.1	111	2	S36263
160	4	57.1	97	2	T51216	233	4	57.1	111	2	S46397
161	4	57.1	97	2	S10385	234	4	57.1	111	2	S19673
162	4	57.1	98	2	S07266	235	4	57.1	111	2	S36274
163	4	57.1	98	2	S3068	236	4	57.1	111	2	S19664
164	4	57.1	98	2	S36047	237	4	57.1	111	2	S36274
165	4	57.1	98	2	S36050	238	4	57.1	111	2	S38497
166	4	57.1	98	2	S36048	239	4	57.1	112	1	L1HUNA
167	4	57.1	98	2	G69336	240	4	57.1	112	1	L1HOMM
168	4	57.1	99	2	S3053	241	4	57.1	112	1	L2HUNG
169	4	57.1	99	2	S36055	242	4	57.1	112	1	L6HUNAR
170	4	57.1	99	2	S36059	243	4	57.1	112	2	C44151
171	4	57.1	99	2	S36057	244	4	57.1	112	2	S46395
172	4	57.1	99	2	S36058	245	4	57.1	112	2	S44123
173	4	57.1	99	2	S36056	246	4	57.1	112	2	D44151
174	4	57.1	99	2	S36054	247	4	57.1	112	2	S31515
175	4	57.1	99	2	AD3031	248	4	57.1	112	2	S31515

GenCore version 5.1.9  
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## Om protein - protein search, using sw model

Run on: October 13, 2005, 01:10:37 ; Search time 300 Seconds

21.584 Million cell updates/sec (without alignments)

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Sequence: 1 YLTQPOS 7

Perfect score: 7

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849397

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

## Post-processing: Listing first 1000 summaries

Database : UniProt 7.2-\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85.7	189	2	Q4SGH9_TETNG	Q4sgbh9 tetraodon n
2	85.7	192	1	KBNS1_BRARE	Q5d9g1 brachydanio
3	85.7	216	2	P90610_TRIPO	Q5dt17 photobacter
4	85.7	227	2	P90610_TRIPO	Q5dt17 tririchromo
5	85.7	230	2	Q4ZPB1_PSEU2	Q5f855 vibrio chol
6	85.7	241	1	RLUE_VIBCH	Q8cinc9 rattus norv
7	85.7	362	1	RFFPL_RAT	Q4UFX1_theliera
8	85.7	453	2	Q4UFX1_THEAN	Q6nk88 theliera a
9	85.7	537	2	Q6NK88_CORDI	Q6nk88 corynebacte
10	85.7	546	2	Q3AVX9_SYNPS	Q3avx9 synchococc
11	85.7	562	2	Q34BP1_RHOE	Q34bp1 rhodopseudo
12	85.7	580	2	Q4SYU1_ATPAN	Q4syu1 tetraodon n
13	85.7	693	2	Q4UH42_ATPAN	Q4uh42 theliera a
14	85.7	698	2	Q4NBP1_ATPAB	Q4nbp1 theliera p
15	85.7	732	2	Q5PMM4_CHLAM	Q515m4 chlamydothi
16	85.7	740	2	Q5PMM4_CHLAM	Q4huy7 gibberella
17	85.7	745	2	Q5PMM4_CHLAM	Q4hzb1 rhodopseudo
18	85.7	877	2	Q54108_DICDI	Q54y08 dictyosteli
19	85.7	1035	2	Q4Hzb9_GIBZE	Q4uh42 theliera a
20	85.7	1136	2	Q6MBV2_PARW	Q6mbv2 parachlamyd
21	85.7	1135	2	Q8M147_DROME	Q8ml47 drosophilid
22	85.7	1375	2	Q94337_DROME	Q94537 drosophilida
23	85.7	1526	2	Q94538_DROME	Q94538 drosophilida
24	85.7	1525	2	Q9VED5_DROME	Q9v6d5 drosophilida
25	85.7	113	2	Q9BDQ2_PANTR	Q9bdq2 pan troglob
26	85.7	45	2	Q3ME10_ANAVT	Q3me10 anabena va
27	71.4	70	2	Q673B6_MOUSE	Q675b6 mus musculu
28	71.4	72	2	Q50370_MYCPN	Q50370 mycoplasma
29	71.4	75	2	Q65978_RHOB	Q65978 roseovariu
30	71.4	87	2	Q82V02_NITROSOM	Q82v02 nitrosomona
31	71.4	91	2	Q322X6_SHIBS	Q322x6 shigella bo

105	5	71.4	209	2	077039_BOMMO	077039 bombyx mori	178	5	71.4	279	2	Q9R75_STRCO	streptomyce
106	5	71.4	209	2	Q51227_ENTHI	Q51227 entamoeba h	179	5	71.4	282	2	Q5RH54_BRARE	brachydanio
107	5	71.4	209	2	Q30XA4_DESOG	Q30XA4 desulfovibr	180	5	71.4	283	2	Q26604_ACHISEOMA	achistosoma
108	5	71.4	211	2	Q320C0_SHIBS	Q320C0 shigella bo	181	5	71.4	284	1	Q5AT53_SCIMA	scima
109	5	71.4	212	2	Q518A7_ENTHI	Q518A7 entamoeba h	182	5	71.4	284	2	Q5AT53_ASPIRILLUS	aspergillus
110	5	71.4	212	2	Q70YI6_GIALA	Q70YI6 giardia lam	183	5	71.4	285	2	Q4AGR9_ECHENI	echeni
111	5	71.4	213	2	Q3B288_PELLD	Q3B288 pelodictyon	184	5	71.4	287	2	Q3IC24_PSEHT	pseudoalter
112	5	71.4	214	2	Q41877_MAIZE	Q41877 zea mays (m	185	5	71.4	288	2	Q8X0N6_NEODCR	neodcr
113	5	71.4	215	1	Y1650_HAEDE	Y1650 haemophilus	186	5	71.4	289	2	Q48RA0_PSE14	pseudomonas
114	5	71.4	216	2	Q5FQZ3_GLUOX	Q5FQZ3 gluconobact	187	5	71.4	289	2	Q73EP9_BACCI	bacillus ce
115	5	71.4	218	2	Q3RV01_RALME	Q3RV01 ralstonia m	188	5	71.4	289	2	Q8JG31_CHICK	chick
116	5	71.4	218	2	Q4V0T4_BACCZ	Q4V0T4 bacillus ce	189	5	71.4	290	2	Q4HWS1_GIBZE	gibberella
117	5	71.4	219	2	Q9VQJ8_DROME	Q9VQJ8 drosophila	190	5	71.4	290	2	Q3GBD3_SYNTHOMO	synthphomo
118	5	71.4	222	1	Q5B8V3_EMENI	Q5B8V3 emenia	191	5	71.4	290	2	Q4ZU27_PSEU2	pseudomonas
119	5	71.4	223	2	Q7NE50_GLOVI	Q7NE50 gloeobacter	192	5	71.4	291	1	YXJO_BACSU	bacillus su
120	5	71.4	224	1	SNC2_HUMAN	041735 homo sapien	193	5	71.4	292	2	Q845T3_VIBVU	vibrio vuln
121	5	71.4	227	2	Q8BNX8_MOUSE	Q8BNX8 mus musculus	194	5	71.4	292	2	Q8D5B1_VIBWU	vibrio vuln
122	5	71.4	228	2	Q9LXK4_ARATH	Q9LXK4 arabidopsis	195	5	71.4	292	2	Q8E861_SHEWANELLA	shewanellea
123	5	71.4	229	1	ISPD_NEIMA	Q9JTM3 neisseria m	196	5	71.4	292	2	Q9P877_GALLUS	gallus gall
124	5	71.4	229	1	ISPD_NEIMB	Q5ZP99 angiococcus	197	5	71.4	293	2	Q2X6T1_SHEWANELLA	shewanellea
125	5	71.4	223	2	Q7NE50_GLOVI	Q7NE50 gloeobacter	198	5	71.4	294	2	Q2ZG92_SHEPU	shewanellea
126	5	71.4	229	1	Q5F829_NEIG1	Q5F829 neisseria g	199	5	71.4	294	2	Q3N3U5_9DELT	syntrophobac
127	5	71.4	230	2	Q3KGM8_PSEPP	Q3KGM8 pseudomonas	200	5	71.4	295	1	RPSC_MYKZA	mykococcus
128	5	71.4	230	2	Q4KG55_PSEPP	Q4KG55 pseudomonas	201	5	71.4	295	2	Q8J2Q9_GIBMO	gibberella
129	5	71.4	230	2	Q3V3H7_MOUSE	Q3V3H7 mus musculus	202	5	71.4	295	2	Q9PB79_CHICK	chick
130	5	71.4	234	1	ZEAL_MAIZE	P02859 zea mays (m	203	5	71.4	295	2	Q7W7A4_BORPA	bordetella
131	5	71.4	234	1	ZEAL_MAIZE	P06675 zea mays (m	204	5	71.4	295	2	Q7W7P1_BORBR	bordetella
132	5	71.4	234	1	ZEAL_MAIZE	P08416 zea mays (m	205	5	71.4	295	2	Q7W7P1_BORBR	bordetella
133	5	71.4	234	2	Q946V6_MAIZE	Q946V6 zea mays (m	206	5	71.4	295	2	Q4K9N0_PSEPS	pseudomonas
134	5	71.4	234	2	Q9AXJ9_9BURK	Q4AXJ9 polaromonas	207	5	71.4	297	2	Q62mN9_DEBHA	debaryomyce
135	5	71.4	235	2	Q67724_TILLE	Q6724 beryx spien	208	5	71.4	298	2	Q64316_ARABATH	arabidopsis
136	5	71.4	237	2	Q31IKM9_PSEHT	Q31IKM9 PSEHT	209	5	71.4	298	2	Q7MC82_VIBVY	vibrio vuln
137	5	71.4	239	2	Q9XVA0_CAEHT	Q9XVA0 caenorhabdi	210	5	71.4	299	2	Q4H5D9_NEDIO	deinococcus
138	5	71.4	240	2	Q4CHF5_CLOTR	Q4CHF5 clostridium	211	5	71.4	299	2	Q3K3Y5_PSEPP	pseudomonas
139	5	71.4	242	2	Q2J5U5_9ACTO	Q2J5U5 9actin	212	5	71.4	299	2	RNH3_HLCV	chlamydom
140	5	71.4	246	2	Q8BYR6_LACTPL	Q8BYR6 lactobacill	213	5	71.4	299	2	Q2W9E6_MACSA	magnetotipir
141	5	71.4	248	1	LEC2_CTVTS	P2925 cytis s	214	5	71.4	299	2	Q3C5U8_ALKALI	alkaliphilu
142	5	71.4	248	1	QAH9K4_9DECI	Q419K4 deinococcus	215	5	71.4	299	2	Q5HVN7_CAMJE	campylobact
143	5	71.4	249	2	Q890D4_9ACTP	Q890d4 lactobacill	216	5	71.4	300	2	Q82S2A7_NITBU	nitrosonoma
144	5	71.4	249	2	Q4CHF5_CLOTR	Q4CHF5 clostridium	217	5	71.4	300	2	Q50M40_ENTHI	entamoeba h
145	5	71.4	250	2	Q4DBL2_TRYCR	Q4db12 trypanoforma	218	5	71.4	300	1	Q871B9_VIBPA	vibrio para
146	5	71.4	250	2	Q517R9_ENTHI	Q517R9 entamoeba h	219	5	71.4	303	2	Q7F131_ORVSA	oryza sativ
147	5	71.4	251	2	Q2SYPB_BURTH	Q2SYPB burkholderi	220	5	71.4	303	2	Q9PNP5_CAMJE	campylobact
148	5	71.4	252	2	Q2B00E8_ASPOR	Q2B00E8 aspor	221	5	71.4	303	2	Q2T2C7_BURTH	burkholderi
149	5	71.4	252	2	Q4DEC9_TRYCR	Q4dec9 trypanoforma	222	5	71.4	304	2	Q82S45_NITBU	nitrosonoma
150	5	71.4	254	2	Q88SN5_BRAJA	Q88sn5 bradyrhizob	223	5	71.4	304	2	Q8V544_DROMB	drosophila
151	5	71.4	254	2	Q7Q9R3_ALNOGA	Q7q9r3 anophelis	224	5	71.4	305	2	Q50P71_HUMAN	entamoeba h
152	5	71.4	256	2	Q8XMB6_RALCET	Q8xmb6 erwinia car	225	5	71.4	305	2	Q831A7_ASHIGELLA	ashigella fl
153	5	71.4	258	2	Q7V1A4_HEILHP	Q7v1a4 ralstonia s	226	5	71.4	305	2	Q3XH27_NPROT	proteobac
154	5	71.4	258	2	Q8GQYS_SYNEL	Q5hkp4 staphylococ	227	5	71.4	310	1	YCJY_ECOLI	escherichia
155	5	71.4	258	2	Q8CTV9_STAES	Q9rvs8 deinococcus	228	5	71.4	310	2	Q5QF71_HUMAN	homosapien
156	5	71.4	260	2	Q8CKW8_RHET	Q8ckw8 rhizobium e	229	5	71.4	310	2	Q3Z177_SHISS	dictyospha
157	5	71.4	261	2	Q6D8F6_ERWCET	Q6d8f6 erwinia car	230	5	71.4	310	2	Q8XBM5_ECOL6	escherichia
158	5	71.4	266	2	Q8XMB6_RALCET	Q8xmb6 ralstonia s	231	5	71.4	310	2	Q8FBH8_LLEIMA	leishmania
159	5	71.4	261	2	Q41909_STAHJ	Q41909 staphylococ	232	5	71.4	311	2	Q5QF71_HUMAN	homosapien
160	5	71.4	261	2	Q5hkp4_STAEQ	Q9rvs8 staphylococ	233	5	71.4	311	2	Q54G10_DICDI	dictyospha
161	5	71.4	261	2	Q8CTU9_STAES	Q8ctu9 staphylococ	234	5	71.4	311	2	Q4LY78_NBURK	burkholderi
162	5	71.4	264	2	Q9H314_9ACTO	Q9h3144 nocardioide	235	5	71.4	311	2	Q3Z177_SHISS	shigella so
163	5	71.4	264	2	Q8B753_XYLFT	Q8b753 xylella fast	236	5	71.4	311	2	Q3XH27_NPROT	proteobacter
164	5	71.4	266	2	Q43J76_9CHLB	Q43j76 chlorobium	237	5	71.4	313	2	Q92H27_THDE	thiobacillu
165	5	71.4	270	2	Q31IG2_MOUSE	Q31ig2 mus musculus	238	5	71.4	313	2	Q3SPM8_THLDA	leishmania
166	5	71.4	258	2	Q8PUV4_9PERC	Q8puv4 channa sp	239	5	71.4	314	2	Q44950_SYNCHOC	synchococc
167	5	71.4	261	2	Q8CTU9_ZEUFKA	Q8ctu9 zeus faber	240	5	71.4	314	2	Q44950_CHRSL	chromohalob
168	5	71.4	271	2	Q3KQF3_9MICC	Q3kf3 arthrobacte	241	5	71.4	315	2	Q2OFU5_EURCH	ehrlichia c
169	5	71.4	272	2	Q3Q309_9GAMB	Q3q309 shewanellea	242	5	71.4	315	2	Q3Q377_PSEPT	silicibacte
170	5	71.4	272	2	Q604A3_METCA	Q604a3 methyloco	243	5	71.4	317	2	Q3WWD7_9RH12	mesorhizobi
171	5	71.4	273	2	Q8ZSP1_PYRAE	Q8zsp1 pyrobaculum	244	5	71.4	317	2	Q5SNM20_THEBT8	thermus the
172	5	71.4	273	2	Q6C124_TARLLA	Q6c124 yarrowia la	245	5	71.4	317	2	Q72Gh7_THEBT2	thermus the
173	5	71.4	274	2	Q2T2D2_RHOPA	Q2t2d2 rhodospaudo	246	5	71.4	318	2	Q2T3T5_BURTH	burkholderi
174	5	71.4	275	2	Q3QKZ2_HUMAN	Q3kqz2 homo sapien	247	5	71.4	318	2	Q3JGJB8_BURP1	burkholderi
175	5	71.4	276	2	Q8B5N2_STRAW	Q8b5n2 streptomyce	248	5	71.4	318	2	Q62AE1_BURMA	burkholderi
176	5	71.4	277	2	Q5B8W7_VIBEF1	Q5b8w7 vibrio fisc	249	5	71.4	318	2	Q63N00_BURPS	burkholderi
177	5	71.4	279	2	Q7NNH8_GLOVI	Q7nnh8 gloeobacter	250	5	71.4	318	2	Q9AA52_CAUCR	caulobacter

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:00:06 ; Search time 41 Seconds

(without alignments) 16.427 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37  
Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62

Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR 80.0

1: PIR1;\*

2: PIR2;\*

3: PIR3;\*

4: PIR4;\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	89.2	331	2 F69025	ATP phosphoribosyl
2	32	86.5	264	2 B71448	hypothetical prote
3	32	86.5	539	2 I49065	lymphoid-restricte
4	32	86.5	921	2 A33718	retinoblastoma pro
5	32	86.5	928	1 RBHU	retinoblastoma-888
6	31	83.8	284	2 S27843	homeotic protein s
7	31	83.8	538	2 B8325	probable gamma-glu
8	30	81.1	290	2 A82236	pseudouridine synth
9	30	81.1	528	2 G70055	probable choline d
10	30	81.1	645	2 T25324	hypothetical prote
11	30	81.1	705	2 BB82044	guanosine-3', 5'-bi
12	30	81.1	980	2 T49570	hypothetical prote
13	30	81.1	1205	2 C84848	hypothetical prote
14	30	81.1	12075	2 T13822	frazzled gene prot
15	30	81.1	14483	2 T19751	hypothetical prote
16	30	81.1	15262	2 T13823	frazzled gene prot
17	29	78.4	214	2 S21669	19K zein precursor
18	29	78.4	229	2 T33141	hypothetical prote
19	29	78.4	234	1 Z12M3	19K zein precursor
20	29	78.4	234	1 Z12M1	19K zein precursor
21	29	78.4	234	2 S03417	19K zein precursor
22	29	78.4	248	2 AB1941	hypothetical prote
23	29	78.4	263	2 A5443	beta-lactamase (EC
24	29	78.4	263	2 S2329	beta-lactamase (EC
25	29	78.4	291	2 S42075	beta-lactamase (EC
26	29	78.4	294	2 S19006	beta-lactamase (EC
27	29	78.4	327	2 T3452	G protein pathway
28	29	78.4	382	1 MFN241	matrix protein - 6
29	29	78.4	402	2 B75297	dipeptidyl peptida

30	78.4	2 D86717	2	hypothetical prote
31	78.4	2 A96555	2	coproporphyrinogen
32	78.4	2 S75657	2	probable flavoprot
33	78.4	2 S74578	2	probable oligope
34	78.4	2 E64820	2	hypothetical prote
35	78.4	2 D90742	2	hypothetical prote
36	78.4	2 G85592	2	holocytochrome c-t
37	78.4	2 T10105	2	hypothetical prote
38	78.4	2 S75772	2	hypothetical prote
39	78.4	2 G82875	2	retrovirus-related
40	78.4	2 S36422	2	RNA-directed DNA p
41	78.4	2 T10540	2	RNA-directed DNA p
42	78.4	2 T10743	2	retrovirus-related
43	78.4	2 C47759	2	thyrotropin beta c
44	78.4	2 A29479	2	4-diphosphocytidyl
45	78.4	2 G64471	2	cell division prote
46	78.4	2 T49820	2	hypothetical prote
47	78.4	2 T06972	2	hypothetical prote
48	78.4	2 H64022	2	hypothetical prote
49	78.4	2 T20603	2	hypothetical prote
50	78.4	2 AC0408	2	4-diphosphocytidyl
51	78.4	2 G64471	2	hypothetical prote
52	78.4	2 T49820	2	hypothetical prote
53	78.4	2 D70080	2	transcription regu
54	78.4	2 T03085	2	ribonuclease homol
55	78.4	2 F81318	2	probable galactosy
56	78.4	2 T34112	2	hypothetical prote
57	78.4	2 AC1867	2	hypothetical prote
58	78.4	2 E90867	2	hypothetical prote
59	78.4	2 DB5751	2	hypothetical prote
60	78.4	2 B64882	2	hypothetical prote
61	78.4	2 G87342	2	hypothetical prote
62	78.4	2 A81399	2	hypothetical prote
63	78.4	2 T47427	2	hypothetical prote
64	78.4	2 T45277	2	hypothetical prote
65	78.4	2 T10801	2	GDP dissociation i
66	78.4	2 T07613	2	replication initia
67	78.4	2 E87613	2	pilus assembly pro
68	78.4	2 JC7539	2	beta-glucosidase (
69	78.4	2 T00329	2	hypothetical prote
70	78.4	2 D91239	2	membrane protein [
71	78.4	2 A86087	2	hypothetical prote
72	78.4	2 F65202	2	hypothetical 66.6
73	78.4	2 H70339	2	NADH2 dehydrogenas
74	78.4	2 T43634	2	hypothetical prote
75	78.4	2 T26297	2	probable transposo
76	78.4	2 F85077	2	Glutamin high mole
77	78.4	2 B30843	2	Glutamin high mole
78	78.4	2 JN0689	2	Glutamin, high-mol
79	78.4	2 SJ15720	2	Glutamin, high mole
80	78.4	2 BBWTHW	2	Glutamin, high mol
81	78.4	2 S02262	2	hypothetical prote
82	78.4	2 T43437	2	reverse transcript
83	78.4	2 T16095	2	alanine tRNA ligas
84	78.4	2 S45298	2	hypothetical prote
85	78.4	2 T00781	2	ubiquitinin-protein
86	78.4	2 C70876	2	hypothetical prote
87	78.4	2 S02904	2	oxoglutarate dehyd
88	78.4	2 A49370	2	reverse transcript
89	78.4	2 T01860	2	potassium channel
90	78.4	2 T27083	2	calcium-activated
91	78.4	2 JC7878	2	calcium-activated
92	78.4	2 S38048	2	calcium-regulated
93	78.4	2 S20969	2	Na+/Ca2+ - K+ -exchan
94	78.4	2 T06977	2	hypothetical prote
95	78.4	2 A39800	2	hypothetical prote
96	78.4	2 I49017	2	hypothetical prote
97	78.4	2 A48206	2	hypothetical prote
98	78.4	2 T14593	2	hypothetical prote
99	78.4	2 FB2909	2	hypothetical prote
100	78.4	2 S09811	2	hypothetical prote
101	78.4	2 T15789	2	hypothetical prote
102	78.4	2 T14593	2	hypothetical prote

103	27	73.0	81	2	T03723	reverse transcript	158345
104	27	73.0	92	2	T0365	reverse transcript	1176
105	27	73.0	92	2	T03617	probable retroelement	27
106	27	73.0	93	2	AF2346	probable retroelement	177
107	27	73.0	107	2	AB2853	ABC transport prot	178
108	27	73.0	111	2	T49549	probable RNA helic	179
109	27	73.0	121	2	S24660	Elleggrin - fruit fl	180
110	27	73.0	140	2	PH0134	probable sideropho	181
111	27	73.0	141	2	T31118	transcription coac	182
112	27	73.0	141	2	136310	CREB-binding prote	183
113	27	73.0	143	2	B82228	lysosomal traffick	184
114	27	73.0	154	2	S33873	ORF MSV241 leucine	185
115	27	73.0	180	2	JU0149	precorrin methylne	186
116	27	73.0	182	2	AD2728	homeobox protein -	187
117	27	73.0	194	2	S19141	probable retrovirus-related	188
118	27	73.0	195	2	S77152	reverse transcript	189
119	27	73.0	195	2	AF2347	reverse transcript	190
120	27	73.0	197	2	E97509	reverse transcript	191
121	27	73.0	205	2	S72585	reverse transcript	192
122	27	73.0	205	2	I64155	reverse transcript	193
123	27	73.0	213	2	S67818	reverse transcript	194
124	27	73.0	213	2	B71079	reverse transcript	195
125	27	73.0	214	2	B82942	reverse transcript	196
126	27	73.0	224	2	T47401	reverse transcript	197
127	27	73.0	225	2	E97509	reverse transcript	198
128	27	73.0	274	2	AC2599	reverse transcript	199
129	27	73.0	298	2	JQ1207	reverse transcript	200
130	27	73.0	300	2	B71079	reverse transcript	201
131	27	73.0	331	2	T22042	reverse transcript	202
132	27	73.0	339	2	S61240	reverse transcript	203
133	27	73.0	343	2	E70587	reverse transcript	204
134	27	73.0	343	2	FB8396	reverse transcript	205
135	27	73.0	348	1	HB6386	reverse transcript	206
136	27	73.0	348	1	Z1BPF1	reverse transcript	207
137	27	73.0	348	1	Z1BPFD	reverse transcript	208
138	27	73.0	361	2	Z1BPM3	reverse transcript	209
139	27	73.0	397	2	AH2434	reverse transcript	210
140	27	73.0	397	2	F72072	reverse transcript	211
141	27	73.0	408	2	HB7193	reverse transcript	212
142	27	73.0	426	2	P71220	reverse transcript	213
143	27	73.0	426	2	G75187	reverse transcript	214
144	27	73.0	428	1	Q4ECA0	probable trehalose	215
145	27	73.0	428	2	DB8603	damx protein (ar0B	216
146	27	73.0	428	2	F91157	hypothetical prote	217
147	27	73.0	430	2	AE1803	probable membrane	218
148	27	73.0	430	2	AF1429	aspartate aminotra	219
149	27	73.0	430	2	A99198	probable membrane	220
150	27	73.0	434	2	G82184	probable membrane	221
151	27	73.0	453	2	AG0353	probable membrane	222
152	27	73.0	453	2	G96695	sugar binding prot	223
153	27	73.0	461	2	D87751	sugar binding prot	224
154	27	73.0	469	2	A45728	hypothetical prote	225
155	27	73.0	491	2	T26594	membrane protein r	226
156	27	73.0	492	2	S55536	phal protein precu	227
157	27	73.0	502	2	T28851	probable membrane	228
158	27	73.0	705	2	CB4406	hypothetical prote	229
159	27	73.0	805	2	G95151	conserved hypothet	230
160	27	73.0	805	2	D98116	respiratory burst	231
161	27	73.0	835	2	T45721	hypothetical prote	232
162	27	73.0	835	2	A46962	phycobilisome link	233
163	27	73.0	883	2	T05848	hypothetical prote	234
164	27	73.0	883	2	T2536	hypothetical prote	235
165	27	73.0	883	2	T46950	hypothetical prote	236
166	27	73.0	883	2	G97780	protein kinase kin	237
167	27	73.0	884	2	S67660	protein kinase kin	238
168	27	73.0	885	2	T45053	sucrose synthase [	239
169	27	73.0	891	2	AH1938	respiratory burst	240
170	27	73.0	891	2	DB4442	phycobilisome link	241
171	27	73.0	926	2	T01167	hypothetical prote	242
172	27	73.0	961	2	T24643	hypothetical prote	243
173	27	73.0	973	2	T42634	connectin/citin -	244
174	27	73.0	1021	2	A10201	beta-galactosidase	245
175	27	73.0	1060	2		conserved hypothet	246

Result No.	Score	Query Match	Length	DB ID	Description
1	3.3	89.2	87	4	US-10-425-115-291176
2	3.3	89.2	119	4	US-10-425-115-124207
3	3.3	89.2	251	4	US-10-319-799-68
4	3.3	89.2	331	4	US-10-369-493-1104
5	3.3	89.2	415	5	US-10-501-282-2354
6	3.3	89.2	503	5	US-10-501-282-2356
7	3.3	89.2	717	5	US-10-501-282-2358
8	3.2	86.5	264	3	US-10-739-930-3322
9	3.2	86.5	781	3	US-09-469-522-37
10	3.2	86.5	815	5	US-10-732-923-15103
11	3.2	86.5	816	3	US-09-469-522-4
12	3.2	86.5	832	3	US-09-469-522-35
13	3.2	86.5	851	3	US-09-469-522-33
14	3.2	86.5	851	3	US-09-469-522-39
15	3.2	86.5	859	3	US-09-469-522-47
16	3.2	86.5	871	3	US-09-469-522-49
17	3.2	86.5	874	3	US-09-469-522-31
18	3.2	86.5	882	5	US-10-732-923-15123
19	3.2	86.5	895	3	US-09-469-522-29
20	3.2	86.5	897	3	US-09-469-522-41
21	3.2	86.5	899	5	US-10-732-923-15104
22	3.2	86.5	921	5	US-10-732-923-15102
23	3.2	86.5	921	5	US-10-732-923-15102
24	3.2	86.5	928	3	US-09-758-007-3
25	3.2	86.5	928	3	US-09-469-522-8
26	3.2	86.5	928	3	US-09-469-522-2
27	3.2	86.5	928	3	US-09-469-522-51
28	86.5	928	3	US-09-860-286-8	
29	86.5	928	3	US-09-880-286-8	
30	86.5	928	4	US-10-028-726-2	
31	86.5	928	4	US-10-042-750-8	
32	86.5	928	4	US-10-041-510-8	
33	86.5	928	4	US-10-048-765A-49	
34	86.5	928	5	US-10-076-363-8	
35	86.5	928	5	US-10-072-152-124	
36	86.5	928	5	US-10-072-923-152-125	
37	86.5	928	5	US-10-072-923-152-126	
38	86.5	928	5	US-10-072-923-152-127	
39	86.5	928	6	US-10-042-750-8	
40	86.5	928	6	US-11-030-594-8	
41	86.5	928	6	US-11-001-801-8	
42	83.8	881	4	US-10-056-761-15087	
43	83.8	128	5	US-10-050-763-32334	
44	83.8	228	4	US-10-057-701-32911	
45	83.8	339	4	US-10-082-122A-45942	
46	83.8	562	4	US-10-032-763-7639	
47	83.8	1047	6	US-11-097-143-29241	
48	81.1	95	4	US-10-024-593-268773	
49	81.1	106	4	US-10-025-115-339336	
50	81.1	162	4	US-10-025-114-45986	
51	81.1	175	4	US-10-025-115-197546	
52	81.1	341	5	US-10-050-822-822	
53	81.1	345	5	US-10-001-282-824	
54	81.1	437	4	US-10-025-114-42857	
55	81.1	488	4	US-10-025-115-263721	
56	81.1	501	4	US-10-025-114-45986	
57	81.1	528	4	US-10-022-122A-64520	
58	81.1	528	4	US-10-022-122A-64520	
59	81.1	538	4	US-10-026-18	
60	81.1	705	4	US-10-022-122A-64520	
61	81.1	738	4	US-10-072-363-194	
62	81.1	738	4	US-10-022-122A-64520	
63	81.1	1375	3	US-09-808-602-66	
64	81.1	1375	3	US-09-800-730-194	
65	81.1	1526	6	US-11-097-143-18609	
66	78.4	10	10	US-09-087-345-8	
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68	78.4	10	6	US-11-220-407-8	
69	78.4	39	5	US-10-042-533-402	
70	78.4	40	4	US-10-099-747-194	
71	78.4	40	4	US-10-099-747-194	
72	78.4	40	5	US-10-079-183-194	
73	78.4	49	4	US-10-024-049-4292	
74	78.4	55	4	US-10-025-115-311628	
75	78.4	56	4	US-10-024-593-20987	
76	78.4	66	4	US-10-025-115-31144	
77	78.4	66	4	US-10-025-115-211727	
78	78.4	67	4	US-10-025-115-32548	
79	78.4	69	4	US-10-025-115-33261	
80	78.4	79	4	US-10-025-115-26249	
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82	78.4	72	4	US-10-025-115-25146	
83	78.4	73	4	US-10-025-115-20807	
84	78.4	74	4	US-10-025-115-302677	
85	78.4	76	4	US-10-025-115-302677	
86	78.4	77	4	US-10-025-115-311628	
87	78.4	78	4	US-10-025-115-311628	
88	78.4	81	5	US-10-025-115-31171	
89	78.4	83	4	US-10-025-115-305330	
90	78.4	94	4	US-10-025-115-329601	
91	78.4	97	4	US-10-025-115-31880	
92	78.4	99	5	US-10-025-115-53129	
93	78.4	103	4	US-10-025-115-37760	
94	78.4	108	4	US-10-025-115-57989	
95	78.4	111	4	US-10-025-115-33035	
96	78.4	112	4	US-10-025-115-329601	
97	78.4	115	4	US-10-025-115-22740	
98	78.4	117	4	US-10-025-115-335020	
99	78.4	117	4	US-10-025-115-336635	
100	78.4	118	4	US-10-025-115-292683	

### SUMMARIES

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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113	29	78.4	139	4	US-10-425-115-323239	Sequence 232139,	224	78.4	US-10-145-124A-162
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117	29	78.4	154	4	US-10-425-115-224488	Sequence 224488,	224	78.4	US-10-164-829A-162
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131	29	78.4	208	4	US-10-425-115-298337	Sequence 298337,	204	78.4	US-10-172-039A-162
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138	29	78.4	224	3	US-09-978-609A-162	Sequence 162,	211	78.4	US-10-013-919A-162
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98	5	71.4	US-11-348-413-111789	Sequence 111789,	Sequence 710, App
99	5	71.4	US-11-348-413-111790	Sequence 111790,	Sequence 800, App
100	5	71.4	US-11-348-413-111791	Sequence 111791,	Sequence 801106,
101	5	71.4	US-11-348-413-111792	Sequence 111792,	Sequence 142167,
102	5	71.4	US-11-348-413-112095	Sequence 112095,	Sequence 14684, A
103	5	71.4	US-11-348-413-112101	Sequence 112101,	Sequence 15982, A
104	5	71.4	US-11-348-413-112102	Sequence 112102,	Sequence 5099, AP
c 105	5	71.4	US-11-348-413-112097	Sequence 112097,	Sequence 5096, AP
c 106	5	71.4	US-11-348-413-112098	Sequence 112098,	Sequence 5097, AP
c 107	5	71.4	US-11-348-413-112099	Sequence 112099,	Sequence 5098, AP
c 108	5	71.4	US-11-348-413-112100	Sequence 112100,	Sequence 5099, AP
c 109	5	71.4	US-11-348-413-112101	Sequence 112101,	Sequence 5100, AP
c 110	5	71.4	US-11-348-413-112102	Sequence 112102,	Sequence 5101, AP
c 111	5	71.4	US-11-348-413-112097	Sequence 112097,	Sequence 5102, AP
c 112	5	71.4	US-11-348-413-112098	Sequence 112098,	Sequence 5103, AP
c 113	5	71.4	US-11-348-413-112099	Sequence 112099,	Sequence 5104, AP
c 114	5	71.4	US-11-348-413-112100	Sequence 112100,	Sequence 5105, AP
c 115	5	71.4	US-11-348-413-112101	Sequence 112101,	Sequence 5106, AP
c 116	5	71.4	US-11-348-413-112102	Sequence 112102,	Sequence 5107, AP
c 117	5	71.4	US-11-348-413-112103	Sequence 112103,	Sequence 5108, AP
c 118	5	71.4	US-11-348-413-112104	Sequence 112104,	Sequence 5109, AP
c 119	5	71.4	US-11-348-413-112105	Sequence 112105,	Sequence 5110, AP
c 120	5	71.4	US-11-348-413-112106	Sequence 112106,	Sequence 5111, AP
c 121	5	71.4	US-11-348-413-112107	Sequence 112107,	Sequence 5112, AP
c 122	5	71.4	US-11-348-413-112108	Sequence 112108,	Sequence 5113, AP
c 123	5	71.4	US-11-348-413-112109	Sequence 112109,	Sequence 5114, AP
c 124	5	71.4	US-11-348-413-112110	Sequence 112110,	Sequence 5115, AP
c 125	5	71.4	US-11-348-413-112111	Sequence 112111,	Sequence 5116, AP
c 126	5	71.4	US-11-348-413-112112	Sequence 112112,	Sequence 5117, AP
c 127	5	71.4	US-11-348-413-112113	Sequence 112113,	Sequence 5118, AP
c 128	5	71.4	US-11-348-413-112114	Sequence 112114,	Sequence 5119, AP
c 129	5	71.4	US-11-348-413-112115	Sequence 112115,	Sequence 5120, AP
c 130	5	71.4	US-11-348-413-112116	Sequence 112116,	Sequence 5121, AP
c 131	5	71.4	US-11-348-413-112117	Sequence 112117,	Sequence 5122, AP
c 132	5	71.4	US-11-348-413-112118	Sequence 112118,	Sequence 5123, AP
c 133	5	71.4	US-11-348-413-112119	Sequence 112119,	Sequence 5124, AP
c 134	5	71.4	US-11-348-413-112120	Sequence 112120,	Sequence 5125, AP
c 135	5	71.4	US-11-348-413-112121	Sequence 112121,	Sequence 5126, AP
c 136	5	71.4	US-11-348-413-112122	Sequence 112122,	Sequence 5127, AP
c 137	5	71.4	US-11-348-413-112123	Sequence 112123,	Sequence 5128, AP
c 138	5	71.4	US-11-348-413-112124	Sequence 112124,	Sequence 5129, AP
c 139	5	71.4	US-11-348-413-112125	Sequence 112125,	Sequence 5130, AP
c 140	5	71.4	US-11-348-413-112126	Sequence 112126,	Sequence 5131, AP
c 141	5	71.4	US-11-348-413-112127	Sequence 112127,	Sequence 5132, AP
c 142	5	71.4	US-11-348-413-112128	Sequence 112128,	Sequence 5133, AP
c 143	5	71.4	US-11-348-413-112129	Sequence 112129,	Sequence 5134, AP
c 144	5	71.4	US-11-348-413-112130	Sequence 112130,	Sequence 5135, AP
c 145	5	71.4	US-11-348-413-112131	Sequence 112131,	Sequence 5136, AP
c 146	5	71.4	US-11-348-413-112132	Sequence 112132,	Sequence 5137, AP
c 147	5	71.4	US-11-348-413-112133	Sequence 112133,	Sequence 5138, AP
c 148	5	71.4	US-11-348-413-112134	Sequence 112134,	Sequence 5139, AP
c 149	5	71.4	US-11-348-413-112135	Sequence 112135,	Sequence 5140, AP
c 150	5	71.4	US-11-348-413-112136	Sequence 112136,	Sequence 5141, AP
c 151	5	71.4	US-11-348-413-112137	Sequence 112137,	Sequence 5142, AP
c 152	5	71.4	US-11-348-413-112138	Sequence 112138,	Sequence 5143, AP
c 153	5	71.4	US-11-348-413-112139	Sequence 112139,	Sequence 5144, AP
23	8	71.4	US-11-283-550-2199	Sequence 2199, AP	Sequence 1109, AP
23	8	71.4	US-11-283-550-2200	Sequence 2200, AP	Sequence 5098, AP
23	8	71.4	US-11-283-550-220		

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 12, 2006, 20:39:59 ; Search time 2564 Seconds  
 261.875 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Egapext	7.0
Delop	6.0	Delext	7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
 Maximum Match 100%  
 Listing First 1000 summaries

Command line parameters:

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-MODEL:frame+P2N.model -DEV=x1P
-Q=/abs/ABSS/sppow/US12102006_151424_15036/app_query.fasta_1
-DB=/abs/ABSS/sppow/US12102006_151424_15036/app_query.fasta_1
-DB=genEmpl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=-1 -END=-1 -MATRIX=bIlogum62 -TRANS=human40_cdi -LIST=1000
-DOCALIGN=000 -THR SCORE=0 -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTRMT=PT0 -NORM=EXT -HEAPSIZ=500 -MINLEN=0 -MAXLEN=1000000000000 -HOST=abs03p
-USER@US10537649 @CGN_1.1.8328 @runat 12102006_151424_15036 -NCPU=6 -ICPU=3
-NO MMW -NEG SCORE=0 -WAIT 30 -DEVSBLOCK=10 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=7 -FGAPEXT=6 -FGAPOP=6
-YGAPOP=10 -YGAPEXT=6 -DELOP=6
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Database : GenEmpl : \*

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4: 9b-p1:*
5: 9b-pr:*
6: 9b-ro:*
7: 9b-sts:*
8: 9b-sy:*
9: 9b-un:*
10: 9b-vi:*
11: 9b-ov:*
12: 9b-hgt:*
13: 9b-in:*
14: 9b-on:*
15: 9b-ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	37	100.0	21	CQ28007 Sequence
2	37	100.0	2000	AX565658 Sequence
3	37	100.0	44681	AC092520 Ciona sav

77	3.5	94.6	168700	12	AC009115	c 150	91.9	145796	4	AC130598
c 78	3.5	94.6	17911	5	AC354992	c 151	91.9	146492	4	AC136223
c 79	3.5	94.6	177738	5	AC021593	c 152	91.9	146958	12	CP573437
c 80	3.5	94.6	18226	15	CP000035	c 153	91.9	148720	12	BK527319
c 81	3.5	94.6	183321	12	AC173169	c 154	91.9	151772	6	AC109294
c 82	3.5	94.6	190171	12	AC149270	c 155	91.9	151863	12	AC179790
c 83	3.5	94.6	201661	12	AC171488	c 156	91.9	152476	12	AP001659
c 84	3.5	94.6	202879	12	AC135648	c 157	91.9	152951	5	AC026371
c 85	3.5	94.6	214494	15	SFPWR100	c 158	91.9	153178	12	AC009929
c 86	3.5	94.6	214496	15	CP000039	c 159	91.9	153713	6	AC119889
c 87	3.5	94.6	215956	11	CR751334	c 160	91.9	154959	6	AL662881
c 88	3.5	94.6	221493	12	AC098143	c 161	91.9	155410	12	AC179303
c 89	3.5	94.6	221118	15	AF386526	c 162	91.9	155451	12	AC067774
c 90	3.5	94.6	221851	15	AF348706	c 163	91.9	155547	6	AC132595
c 91	3.5	94.6	220339	12	AC111941	c 164	91.9	155691	12	AC023214
c 92	3.5	94.6	226546	6	AL807234	c 165	91.9	156500	12	CR92441
c 93	3.5	94.6	235571	12	AC130022	c 166	91.9	157652	5	AC135851
c 94	3.5	94.6	233372	12	AC098033	c 167	91.9	158039	6	AL663110
c 95	3.5	94.6	238075	12	AC127907	c 168	91.9	160799	12	AC177126
c 96	3.5	94.6	252222	12	AC108271	c 169	91.9	161154	6	AC116868
c 97	3.5	94.6	253390	12	AC172070	c 170	91.9	164715	12	AC161706
c 98	3.5	94.6	264661	12	AC103215	c 171	91.9	166166	5	AC079380
c 99	3.4	91.9	376	2	C0441235	c 172	91.9	166930	11	AC146690
c 100	3.4	91.9	410	4	AB016143	c 173	91.9	166976	12	AC034274
c 101	3.4	91.9	622	7	BV354507	c 174	91.9	167589	12	AC176810
c 102	3.4	91.9	892	2	AR671031	c 175	91.9	168025	12	AC024364
c 103	3.4	91.9	1981	5	AK056166	c 176	91.9	168197	6	AC137511
c 104	3.4	91.9	2000	2	AK509675	c 177	91.9	168293	12	AC018397
c 105	3.4	91.9	2000	2	AX652380	c 178	91.9	168930	12	AC137940
c 106	3.4	91.9	2229	7	BV178520	c 179	91.9	169243	5	AC104816
c 107	3.4	91.9	2422	5	BC063873	c 180	91.9	169310	6	AC119259
c 108	3.4	91.9	2448	2	AX684874	c 181	91.9	171790	6	BK537331
c 109	3.4	91.9	2959	5	AK092222	c 182	91.9	172476	5	AC007736
c 110	3.4	91.9	3221	11	BC084750	c 183	91.9	172507	5	AC092960
c 111	3.4	91.9	3740	4	LS32017	c 184	91.9	172549	12	AC027519
c 112	3.4	91.9	3951	4	AY099660	c 185	91.9	172613	5	AC113398
c 113	3.4	91.9	5379	2	AX345232	c 186	91.9	174923	12	AC023350
c 114	3.4	91.9	14096	15	AE004104	c 187	91.9	175419	12	AC177128
c 115	3.4	91.9	16293	15	AE003150	c 188	91.9	175737	12	AC147487
c 116	3.4	91.9	18120	4	NCOA	c 189	91.9	176692	12	AC164601
c 117	3.4	91.9	18215	13	U97552	c 190	91.9	177771	6	AC115949
c 118	3.4	91.9	30020	13	CBC1208	c 191	91.9	178011	6	AC129572
c 119	3.4	91.9	45962	12	AC066498	c 192	91.9	179888	6	AC102287
c 120	3.4	91.9	84432	4	AC005850	c 193	91.9	179968	12	AC140813
c 121	3.4	91.9	52089	12	CR352281	c 194	91.9	180001	5	AC112196
c 122	3.4	91.9	57073	15	BA000038_18	c 195	91.9	181565	34	AC128628
c 123	3.4	91.9	59652	12	AC137082	c 196	91.9	181589	11	AC14544
c 124	3.4	91.9	6126	5	AL354752	c 197	91.9	183218	6	AC132440
c 125	3.4	91.9	73807	5	AL606530	c 198	91.9	183544	6	AC102132
c 126	3.4	91.9	84345	11	BX936340	c 199	91.9	191946	12	AC177713
c 127	3.4	91.9	80280	12	AC136769	c 200	91.9	189263	12	AC176030
c 128	3.4	91.9	95954	12	AP008104	c 201	91.9	190504	12	AC172252
c 129	3.4	91.9	103822	5	AL353639	c 202	91.9	193857	12	AC145544
c 130	3.4	91.9	101000	15	AE015151_38	c 203	91.9	194194	6	AL51488
c 131	3.4	91.9	108176	6	AL845327	c 204	91.9	194156	12	AC182058
c 132	3.4	91.9	110000	15	BA000038_17	c 205	91.9	195733	6	AL928960
c 133	3.4	91.9	110000	4	AP008211_06	c 206	91.9	196152	5	AC021242
c 134	3.4	91.9	124074	5	BH112E0	c 211	91.9	196567	12	AC178103
c 140	3.4	91.9	128898	12	AC147464	c 213	91.9	196916	6	AC164402
c 141	3.4	91.9	133202	5	AL13182	c 214	91.9	197875	11	AC146543
c 142	3.4	91.9	134928	12	AC168497	c 215	91.9	197906	6	AC154422
c 143	3.4	91.9	135301	12	AC175999	c 216	91.9	200910	6	AC083946
c 144	3.4	91.9	137385	12	AC113357	c 217	91.9	201282	6	AC132450
c 145	3.4	91.9	137690	12	AC151647	c 218	91.9	201625	12	AC012144
c 146	3.4	91.9	133302	5	AC108060	c 219	91.9	202686	11	AC146539
c 147	3.4	91.9	142740	6	AC145660	c 220	91.9	203426	6	AC162046
c 148	3.4	91.9	142740	6	AC103674	c 221	91.9	203422	6	AL13863
c 149	3.4	91.9	143111	12	CR626523	c 222	91.9	204899	5	AC117457

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GenCore version 5.1.9									
Copyright (c) 1993 - 2006 Biocceleration Ltd.									
OM protein - nucleic search, using frame_Plus_P2n model									
Run on:	October 12, 2006, 21:08:36	Search time	3103	Seconds					
		(without alignments)							
	189.221	Million cell	updates/sec						
Title:	US-10-537-648-1								
Perfect score:	7	YLTPQPS	7						
Sequence:									
Scoring table:	OLIGOP								
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	Ygapop	60.0	Ygapext	60.0					
	FGapop	60.0	FGapext	7.0					
	Delop	60.0	Delext	60.0					
Searched:	48236798	seqs,	27595665780	residues					
Word size:	1								
Total number of hits satisfying chosen parameters:	96457779								
Minimum DB seq length:	0								
Maximum DB seq length:	20000000000								
Post-processing: Listing first 1000 summaries									
Command line parameters:									
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Database :	EST,*								
	1: gb_est1:*								
	2: gb_est3:*								
	3: gb_est4:*								
	4: gb_est5:*								
	5: gb_est6:*								
	6: gb_htc:*								
	7: gb_est2:*								
	8: gb_est7:*								
	9: gb_est8:*								
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	11: gb_gbs1:*								
	12: gb_gbs2:*								
	13: gb_gbs3:*								
	14: gb_gbs4:*								
Pre. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Match	Length	DB	ID	Description			
1	7	100.0	288	7	BB358863	BB358863			
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3	7	100.0	320	12	CEB53641	CEB53641			
4	7	100.0	331	11	A2240574	A2240574			

c	78	6	85.7	222	14	DU486164	109842109	c	151	6	85.7	310	10	DW164859	CLVY3403.
	79	6	85.7	225	2	BI0363612	PM0-HN007	c	152	6	85.7	313	13	DW0302	HUM05RH11B
	80	6	85.7	227	2	BI297998	UI-R-CV2-	c	153	6	85.7	313	13	CW511846	Shotgun_G
c	81	6	85.7	227	7	BF230266	251788_BA	c	154	6	85.7	314	5	CB956816	DH04G24Z
c	82	6	85.7	228	1	AI254348	QU65C05-X	c	155	6	85.7	314	5	CN23696	WLA051A04
c	83	6	85.7	228	1	AA612429	vo05h04-X	c	156	6	85.7	316	8	CR740891	CR740891
c	84	6	85.7	229	1	AV323627	AV323627	c	157	6	85.7	318	7	BB252401	BB252401
c	85	6	85.7	231	7	BB478527	BB478527	c	158	6	85.7	318	11	BH491636	BOHEK26TR
c	86	6	85.7	232	8	CR519429	CR519429	c	159	5	CD58065	DH04G82A0			
c	87	6	85.7	236	4	BX836501	BX836501	c	160	6	85.7	321	10	RG2114	Ye83806_81
c	88	6	85.7	236	7	AW81701	QV0-ST021	c	161	6	85.7	322	2	BG28330	ux4112.X
c	89	6	85.7	237	1	AI280359	q19ac11.X	c	162	6	85.7	322	13	CL706266	CMHD-GT_1
c	90	6	85.7	238	1	AA014107	mh29f07-X	c	163	6	85.7	324	2	BG210367	RG244238
c	91	6	85.7	238	1	AI370845	ta63112-X	c	164	6	85.7	324	10	CS7801D04	CW511508
c	92	6	85.7	241	5	CK261554	EST07632	c	165	6	85.7	325	13	CW511508	Shotgun_G
c	93	6	85.7	244	2	BG588726	EST90535	c	166	6	85.7	327	1	AA18077	mn08911_F
c	94	6	85.7	247	11	AZ464767	1M0474L16	c	167	6	85.7	327	13	CL631999	CMHD-GT_1
c	95	6	85.7	250	1	AV292176	AV222176	c	168	6	85.7	329	3	BM334523	UI-M-BH2-
c	96	6	85.7	251	3	BQ007023	UI-H-EI1-	c	169	6	85.7	329	5	CD857729	DH04G92ZC0
c	97	6	85.7	252	1	AI94697	wp88510-X	c	170	6	85.7	329	10	FL125	HSC2UB91.n
c	98	6	85.7	252	7	AW6633956	hi78b08-X	c	171	6	85.7	330	11	AZ462826	AZ462826
c	99	6	85.7	252	7	BEB950873	UI-M-BH4-	c	172	6	85.7	331	7	BBS32596	BBS32596
c	100	6	85.7	253	9	DP0176	DM044D12A	c	173	6	85.7	331	7	AN125571	UI-M-BH4-
c	101	6	85.7	254	8	CR462247	CR462247	c	174	6	85.7	333	7	BBS55670	UI-M-BH4-
c	102	6	85.7	254	9	DB0313	HUM061E12B	c	175	6	85.7	333	12	CG485974	OST720659
c	103	6	85.7	255	2	BG374398	UI-R-CV1-	c	176	6	85.7	335	14	CR294455	CR294455
c	104	6	85.7	255	2	EG811010	daF88d06	c	177	6	85.7	336	2	BIO28828	CM0-MT018
c	105	6	85.7	256	10	DW121216	CLR2518.	c	178	6	85.7	336	3	BQ888183	QGF14D20.
c	106	6	85.7	256	7	BP950873	BP950873	c	179	6	85.7	337	1	AA14371	mb65903.X
c	107	6	85.7	258	1	DV414893	NADW050TR	c	180	6	85.7	338	1	AU022166	AU022166
c	108	6	85.7	262	2	BI297375	UI-R-CV2-	c	181	6	85.7	338	11	AZ704781	RPC1-23-2
c	109	6	85.7	263	7	BP1300146	UI-R-CV2-	c	182	6	85.7	338	12	CG577791	OST1214348
c	110	6	85.7	263	7	BP139867	nab71a10.	c	183	6	85.7	340	1	AA237331	EST333893
c	111	6	85.7	264	7	BB1214710	BB1214710	c	184	6	85.7	340	7	BW814070	RC0-ST019
c	112	6	85.7	265	10	DV771843	McClintoc	c	185	6	85.7	340	9	CX562950	UI-M-IB0
c	113	6	85.7	268	12	CE339107	tier-989-	c	186	6	85.7	340	10	DT052161	DT052161
c	114	6	85.7	270	12	CG487381	OS28865	c	187	6	85.7	341	4	BY111013	BY111013
c	115	6	85.7	271	4	CA48913	UI-H-FH1-	c	188	6	85.7	342	2	BF886333	PM3-TN010
c	116	6	85.7	271	9	DB0226	HUM04F09A	c	189	6	85.7	343	4	CB633519	AMGNNUC:N
c	117	6	85.7	274	3	BW069751	im23g12-Y	c	190	6	85.7	343	14	CR136338	Forward_B
c	118	6	85.7	279	1	AA679398	zi73a09.5	c	191	6	85.7	344	1	AA469244	nc63906.8
c	119	6	85.7	279	2	BG759088	602710724	c	192	6	85.7	344	4	BW16886	BW916886
c	120	6	85.7	279	7	AW485727	67446_MAR	c	193	6	85.7	345	7	BH314189	BH314189
c	121	6	85.7	279	7	BB30106	BB30106	c	194	6	85.7	347	1	AA988110	UI-R-C0-h
c	122	6	85.7	280	7	BB112871	BB112871	c	195	6	85.7	347	12	CG487031	CG487031
c	123	6	85.7	285	1	AA468535	ne06g03.5	c	196	6	85.7	349	6	BB314013	BB314013
c	124	6	85.7	285	1	AQ381436	RPC1.1-13	c	197	6	85.7	350	1	AA0310161	mh88c11.r
c	125	6	85.7	286	8	CO873481	BovGen_01	c	198	6	85.7	350	12	CG493227	OS131508
c	126	6	85.7	286	8	CO876640	BovGen_04	c	199	6	85.7	352	10	NT74614	za55a08.s
c	127	6	85.7	288	3	BG204927	IST4344	c	200	6	85.7	353	10	AA008907	W8741e09.s
c	128	6	85.7	288	3	BO848917	QGABH16.Y	c	201	6	85.7	353	12	CE707150	tig-988-
c	129	6	85.7	288	4	BX303555	BX303555	c	202	6	85.7	355	8	CK977658	410397_B
c	130	6	85.7	289	10	DY152116	000508BTN	c	203	6	85.7	356	7	AV775301	AV775301
c	131	6	85.7	289	3	BB510733	BB510733	c	204	6	85.7	357	9	DA719661	DA719661
c	132	6	85.7	290	4	CD077602	MA3-9999U	c	205	6	85.7	357	9	AA647386	VQ77c05.s
c	133	6	85.7	290	11	CD705379	EST21906	c	206	6	85.7	359	1	AA226908	VN31b01.
c	134	6	85.7	290	11	B37454	HS-1043-B2-	c	207	6	85.7	362	12	CG564661	CG564661
c	135	6	85.7	291	7	BF56052	UI-R-E1-f	c	208	6	85.7	363	3	BB84567	BB84567
c	136	6	85.7	291	4	AA291494	zt41909.8	c	209	6	85.7	363	7	BB805097	BB805097
c	137	6	85.7	294	10	DY152116	000508BTN	c	210	6	85.7	363	12	CB760902	tig-988-
c	138	6	85.7	295	1	AA907339	om09b03.5	c	211	6	85.7	365	11	AA719661	DA719661
c	139	6	85.7	295	1	AV141194	AV141194	c	212	6	85.7	365	11	AZ482650	AZ482650
c	140	6	85.7	295	8	CR461685	CR461685	c	213	6	85.7	366	12	CG483920	CG483920
c	141	6	85.7	296	1	AV086855	AV086855	c	214	6	85.7	366	13	CL610380	CMHD-GT_1
c	142	6	85.7	297	2	EG73052	de05b9.9	c	215	6	85.7	367	2	BG068127	H31062A10-1
c	143	6	85.7	298	7	BB458994	BB458994	c	216	6	85.7	367	14	CR148713	Forward_S
c	144	6	85.7	298	1	AA47386	vq81c04.r	c	217	6	85.7	368	1	DO42483	DO42483
c	145	6	85.7	301	1	AQ332796	RPC1-11-4	c	218	6	85.7	369	13	CL569078	CL569078
c	146	6	85.7	305	8	CO886548	BoVgen_14	c	219	6	85.7	370	3	BP386340	BP386340
c	147	6	85.7	306	12	CG561977	OST184001	c	220	6	85.7	370	12	CG513120	CG513120
c	148	6	85.7	308	1	AU150143	AU150143	c	221	6	85.7	372	1	BG959332	BG959332
c	149	6	85.7	308	7	BB280190	BB280190	c	222	6	85.7	372	1	AA642191	AA642191
c	150	6	85.7	310	10	DW164699	CLVY3240.	c	223	6	85.7	372	1	A1216186	A1216186

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1 protein - nucleic search, using frame_Plus_B2n model		2		3		4		5		6		7		8		9		10		11		12		13		14		15		16		17		18		19		20		21		22		23		24		25		26		27		28		29		30		31		32		33		34		35		36		37		38		39		40		41		42		43		44		45		46		47		48		49		50		51		52		53		54		55		56		57		58		59		60		61		62		63		64		65		66		67		68		69		70		71		72		73																																																																																																																																																																																																																																																																																																																																			
Copyright (c) 1993 - 2006 Biocceleration Ltd.		Sequence 1212172,		Sequence 581792,		Sequence 702816,		Sequence 181503,		Sequence 4967 , AP		Sequence 4501 , AP		Sequence 4507 , AP		Sequence 4528 , AP		Sequence 4534 , AP		Sequence 4557 , AP		Sequence 4563 , AP		Sequence 4587 , AP		Sequence 4592 , AP		Sequence 4614 , AP		Sequence 4620 , AP		Sequence 26779 , A		Sequence 2491 , AP		Sequence 2497 , AP		Sequence 2522 , AP		Sequence 2526 , AP		Sequence 2537 , AP		Sequence 2543 , AP		Sequence 2566 , AP		Sequence 2570 , AP		Sequence 2583 , AP		Sequence 2588 , AP		Sequence 2612 , AP		Sequence 2615 , AP		Sequence 2626 , AP		Sequence 2632 , AP		Sequence 2656 , AP		Sequence 2660 , AP		Sequence 2674 , AP		Sequence 2688 , AP		Sequence 2690 , AP		Sequence 166919 ,		Sequence 24706 , A		Sequence 2840 , AP		Sequence 59154 , A		Sequence 105513 ,		Sequence 123375 ,		Sequence 71 , App1		Sequence 69 , App1		Sequence 69 , App1		Sequence 15741 , A		Sequence 279612 ,		Sequence 89021 ,		Sequence 535602 ,		Sequence 535602 ,		Sequence 189830 ,		Sequence 189830 ,		Sequence 760213 ,		Sequence 760214 ,		Sequence 890550 ,		Sequence 174647 ,		Sequence 98852 , A		Sequence 331874 ,		Sequence 187047 ,		Sequence 891889 ,		Sequence 871889 ,		Sequence 871889 ,		Sequence 871889 ,		Sequence 902648 ,																																																																																																																																																																																																																																																																																																																																																					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

470

Sequence 187047,  
Sequence 871889,  
Sequence 902648,  
Sequence 871889,  
Sequence 902648,

description ----- Sequence 581754,

Result  
No  
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C

75	85.7	540	12	US-10-301-480-266050	Sequence 266050,	C 148	85.7	US-09-925-065A-81183	Sequence 81183, A
76	85.7	540	12	US-09-930-213-97	Sequence 87459,	C 149	85.7	US-09-925-065A-67060	Sequence 67060,
C 77	85.7	541	3	US-09-930-213-97	Sequence 97, App1	C 150	85.7	US-10-301-480-182422	Sequence 182422,
C 78	85.7	543	4	US-09-925-065A-793236	Sequence 793236,	C 151	85.7	US-10-301-480-795831	Sequence 795831,
C 79	85.7	543	4	US-09-925-065A-793236	Sequence 793236,	C 152	85.7	US-09-925-065A-367198	Sequence 367198,
C 80	85.7	546	4	US-09-925-065A-397004	Sequence 397004,	C 153	85.7	US-09-925-065A-367198	Sequence 367198,
C 81	85.7	546	5	US-09-925-065A-397004	Sequence 397004,	C 154	85.7	US-09-925-065A-642167	Sequence 642167,
C 82	85.7	547	12	US-10-301-480-405626	Sequence 405626,	C 155	85.7	US-09-925-065A-642167	Sequence 642167,
C 83	85.7	547	12	US-10-301-480-464660	Sequence 464660,	C 156	85.7	US-10-027-632-26965	Sequence 26965, A
C 84	85.7	547	12	US-10-301-480-1019035	Sequence 1019035,	C 157	85.7	US-10-027-632-26965	Sequence 26965, A
C 85	85.7	547	12	US-10-301-480-1078069	Sequence 1078069,	C 158	85.7	US-10-027-632-284217	Sequence 284217,
C 86	85.7	547	4	US-09-925-065A-102603	Sequence 102603,	C 159	85.7	US-10-027-632-284217	Sequence 284217,
C 87	85.7	552	5	US-09-925-065A-102603	Sequence 102603,	C 160	85.7	US-09-925-065A-523653	Sequence 523653,
C 88	85.7	552	12	US-10-301-480-247675	Sequence 247675,	C 161	85.7	US-09-925-065A-523653	Sequence 523653,
C 89	85.7	552	12	US-10-301-480-861084	Sequence 861084,	C 162	85.7	US-10-027-632-269650	Sequence 269650,
C 90	85.7	553	4	US-09-925-065A-10779	Sequence 10779, A	C 163	85.7	US-09-925-065A-806980	Sequence 806980,
C 91	85.7	553	5	US-09-925-065A-10779	Sequence 10779, A	C 164	85.7	US-10-437-963-24461	Sequence 24461, A
C 92	85.7	553	12	US-10-301-480-112016	Sequence 112016,	C 165	85.7	US-09-925-065A-804551	Sequence 804551,
C 93	85.7	553	12	US-10-301-480-725255	Sequence 725255,	C 166	85.7	US-09-925-065A-804551	Sequence 804551,
C 94	85.7	555	12	US-10-301-480-202964	Sequence 202964,	C 167	85.7	US-09-925-065A-41773	Sequence 41773, A
C 95	85.7	555	12	US-10-301-480-816373	Sequence 816373,	C 168	85.7	US-09-925-065A-41773	Sequence 41773, A
C 96	85.7	562	4	US-09-925-065A-154126	Sequence 154126,	C 169	85.7	US-09-925-065A-41773	Sequence 41773, A
C 97	85.7	562	4	US-09-925-065A-140117	Sequence 140117,	C 170	85.7	US-10-301-480-143011	Sequence 143011,
C 98	85.7	562	5	US-09-925-065A-154126	Sequence 154126,	C 171	85.7	US-10-301-480-143011	Sequence 143011,
C 99	85.7	562	5	US-09-925-065A-140117	Sequence 140117,	C 172	85.7	US-10-301-480-143011	Sequence 143011,
C 100	85.7	568	4	US-09-925-065A-372545	Sequence 372545,	C 173	85.7	US-10-301-480-756119	Sequence 756119,
C 101	85.7	568	4	US-09-925-065A-372545	Sequence 372545,	C 174	85.7	US-10-301-480-756120	Sequence 756120,
C 102	85.7	571	6	US-10-027-632-273007	Sequence 273007,	C 175	85.7	US-09-738-626-113	Sequence 113, App
C 103	85.7	571	7	US-10-027-632-273007	Sequence 273007,	C 176	85.7	US-10-425-124134	Sequence 124134, A
C 104	85.7	574	3	US-09-864-961-12897	Sequence 12897, A	C 177	85.7	US-10-027-632-25329	Sequence 25329, A
C 105	85.7	575	12	US-10-301-480-501123	Sequence 501123,	C 178	85.7	US-10-027-632-32719	Sequence 32719, A
C 106	85.7	575	12	US-10-301-480-501123	Sequence 501123,	C 179	85.7	US-10-027-632-32719	Sequence 32719, A
C 107	85.7	576	4	US-09-925-065A-507815	Sequence 507815,	C 180	85.7	US-10-027-632-32719	Sequence 32719, A
C 108	85.7	576	4	US-09-925-065A-507815	Sequence 507815,	C 181	85.7	US-10-027-632-32719	Sequence 32719, A
C 109	85.7	576	4	US-09-925-065A-507817	Sequence 507817,	C 182	85.7	US-10-027-632-32719	Sequence 32719, A
C 110	85.7	576	5	US-09-925-065A-507815	Sequence 507815,	C 183	85.7	US-10-027-632-32719	Sequence 32719, A
C 111	85.7	576	5	US-09-925-065A-507815	Sequence 507815,	C 184	85.7	US-10-027-632-32719	Sequence 32719, A
C 112	85.7	576	7	US-09-925-065A-507817	Sequence 507817,	C 185	85.7	US-10-027-632-32719	Sequence 32719, A
C 113	85.7	576	7	US-10-104-901-241	Sequence 241, App	C 186	85.7	US-10-363-345A-26761	Sequence 26761, A
C 114	85.7	588	12	US-10-301-480-536883	Sequence 536883,	C 187	85.7	US-10-363-345A-26762	Sequence 26762, A
C 115	85.7	588	12	US-10-301-480-536883	Sequence 536883,	C 188	85.7	US-10-363-483A-6761	Sequence 6761, A
C 116	85.7	589	4	US-09-925-065A-745719	Sequence 745719,	C 189	85.7	US-09-925-065A-745719	Sequence 745719, A
C 117	85.7	589	5	US-09-925-065A-745719	Sequence 745719,	C 190	85.7	US-10-777-543-7933	Sequence 7933, Ap
C 118	85.7	589	6	US-10-027-632-106921	Sequence 106921,	C 191	85.7	US-10-369-493-1001	Sequence 10401, A
C 119	85.7	589	7	US-10-104-901-241	Sequence 241, App	C 192	85.7	US-10-027-632-104867	Sequence 104867,
C 120	85.7	590	6	US-10-027-632-92408	Sequence 92408, A	C 193	85.7	US-10-027-632-104867	Sequence 104867,
C 121	85.7	590	7	US-10-027-632-92408	Sequence 92408, A	C 194	85.7	US-09-925-065A-6799	Sequence 6799, Ap
C 122	85.7	590	7	US-10-027-632-92408	Sequence 92408, A	C 195	85.7	US-09-925-065A-6799	Sequence 6799, Ap
C 123	85.7	595	4	US-09-925-065A-588388	Sequence 588388,	C 196	85.7	US-10-301-480-108036	Sequence 108036,
C 124	85.7	595	4	US-09-925-065A-588388	Sequence 588388,	C 197	85.7	US-10-777-543-7933	Sequence 7933, Ap
C 125	85.7	595	4	US-09-925-065A-588388	Sequence 588388,	C 198	85.7	US-10-027-632-161624	Sequence 161624,
C 126	85.7	595	5	US-09-925-065A-588388	Sequence 588388,	C 199	85.7	US-09-925-065A-6799	Sequence 6799, Ap
C 127	85.7	596	4	US-09-925-065A-588388	Sequence 588388,	C 200	85.7	US-09-925-065A-6799	Sequence 6799, Ap
C 128	85.7	596	5	US-09-925-065A-588388	Sequence 588388,	C 201	85.7	US-10-027-632-161624	Sequence 161624,
C 129	85.7	596	5	US-09-925-065A-588388	Sequence 588388,	C 202	85.7	US-10-027-632-161624	Sequence 161624,
C 130	85.7	601	4	US-09-925-065A-71483	Sequence 71483,	C 203	85.7	US-10-027-632-161624	Sequence 161624,
C 131	85.7	601	6	US-10-301-480-507815	Sequence 507815,	C 204	85.7	US-10-301-480-115639	Sequence 115639,
C 132	85.7	605	6	US-10-027-632-292050	Sequence 292050,	C 205	85.7	US-10-027-632-292050	Sequence 292050,
C 133	85.7	605	7	US-10-301-480-62-92050	Sequence 292050,	C 206	85.7	US-11-01-206-35	Sequence 35, App1
C 134	85.7	620	12	US-10-301-480-64316	Sequence 46316,	C 207	85.7	US-10-106-698-1246	Sequence 1246, Ap
C 135	85.7	620	12	US-10-301-480-64316	Sequence 46316,	C 208	85.7	US-09-925-065A-712407	Sequence 712407,
C 136	85.7	620	12	US-10-301-480-107725	Sequence 107725,	C 209	85.7	US-09-925-065A-712407	Sequence 712407,
C 137	85.7	620	12	US-10-301-480-107725	Sequence 107725,	C 210	85.7	US-09-925-065A-712408	Sequence 712408,
C 138	85.7	621	4	US-09-925-065A-396556	Sequence 396556,	C 211	85.7	US-09-925-065A-712407	Sequence 712407,
C 139	85.7	621	4	US-09-925-065A-396557	Sequence 396557,	C 212	85.7	US-09-925-065A-712408	Sequence 712408,
C 140	85.7	621	5	US-09-925-065A-396556	Sequence 396556,	C 213	85.7	US-09-925-065A-712407	Sequence 712407,
C 141	85.7	621	5	US-09-925-065A-396557	Sequence 396557,	C 214	85.7	US-09-925-065A-712408	Sequence 712408,
C 142	85.7	632	4	US-09-925-065A-926348	Sequence 926348,	C 215	85.7	US-10-653-047-532	Sequence 532, App
C 143	85.7	632	5	US-09-925-065A-926348	Sequence 926348,	C 216	85.7	US-10-282-122A-41317	Sequence 41317, A
C 144	85.7	633	12	US-10-301-480-543523	Sequence 437523,	C 217	85.7	US-10-301-480-543523	Sequence 437523,
C 145	85.7	633	12	US-10-301-480-1156532	Sequence 1156532,	C 218	85.7	US-10-078-929-37	Sequence 37, App1
C 146	85.7	635	4	US-09-925-065A-81183	Sequence 81183,	C 219	85.7	US-10-301-480-1156532	Sequence 37, App1
C 147	85.7	635	4	US-09-925-065A-672060	Sequence 672060,	C 220	85.7	US-11-031-206-37	Sequence 37, App1



81	6	85.7	132762	3	US-09-954-556-17	Sequence 17, App1	c 154	71.4	US-09-397-787-15	
	c 82	6	85.7	140725	3	US-09-949-016-17074	Sequence 17, App1	c 155	71.4	US-09-248-796A-10517
	c 83	6	85.7	148759	3	US-09-949-016-12266	Sequence 13266, A	c 156	5	US-09-248-796A-10517
	c 84	6	85.7	191078	3	US-09-949-016-12707	Sequence 12707, A	c 157	5	US-09-489-039A-5968
	c 85	6	85.7	190585	3	US-09-949-016-17026	Sequence 17026, A	c 158	5	US-09-248-796A-33747
	c 86	6	85.7	205044	3	US-09-949-016-15851	Sequence 15851, A	c 159	5	US-09-513-999C-20626
	c 87	6	85.7	205044	3	US-09-949-016-15852	Sequence 15852, A	c 160	5	US-09-789-559-28
	c 88	6	85.7	212044	3	US-09-949-016-15853	Sequence 15853, A	c 161	5	US-09-789-559-28
	c 89	6	85.7	211049	3	US-09-949-016-15770	Sequence 15770, A	c 162	5	US-09-700-10971
	c 90	6	85.7	22471	3	US-09-949-016-12387	Sequence 12387, A	c 163	5	US-08-700-637-5
	c 91	6	85.7	22471	3	US-09-949-016-12724	Sequence 12724, A	c 164	5	US-08-559-1792A-9
	c 92	6	85.7	22471	3	US-09-949-016-12725	Sequence 12725, A	c 165	5	US-08-700-637-7
	c 93	6	85.7	305098	3	US-09-949-016-11868	Sequence 11868, A	c 166	5	US-09-490-099B-451
	c 94	6	85.7	302604	3	US-09-949-016-14589	Sequence 14589, A	c 167	5	US-09-513-999C-11016
	c 95	6	85.7	305064	3	US-09-949-016-14589	Sequence 14589, A	c 168	5	US-09-513-999C-2552
	c 96	6	85.7	304533	3	US-09-949-016-15751	Sequence 15371, A	c 169	5	US-09-902-540-8524
	c 97	6	85.7	304533	3	US-09-949-016-13372	Sequence 15372, A	c 170	5	US-09-928-700-637-11
	c 98	6	85.7	308362	3	US-09-949-016-17119	Sequence 17119, A	c 171	5	US-09-201-945-22
	c 99	6	85.7	784431	3	US-09-751-389-3	Sequence 3, App1	c 172	5	US-09-297-648-418
	c 100	6	85.7	1664976	3	US-08-916-421B-1	Sequence 1, App1	c 173	5	US-09-297-648-424
	c 101	6	85.7	1664976	3	US-08-916-421B-1	Sequence 1, App1	c 174	5	US-09-297-648-1483
	c 102	5	71.4	20	3	US-08-117-552-353	Sequence 1, App1	c 175	5	US-09-297-648-1681
	c 103	5	71.4	22	3	US-08-949-014C-10	Sequence 353, App1	c 176	5	US-08-637-794A-22
	c 104	5	71.4	22	3	US-08-859-998-44	Sequence 44, App1	c 177	5	US-08-871-755A-22
	c 105	5	71.4	25	3	US-09-225-228-44	Sequence 44, App1	c 178	5	US-09-201-945-22
	c 106	5	71.4	25	3	US-09-701B-44	Sequence 44, App1	c 179	5	US-09-640-211A-1871
	c 107	5	71.4	25	3	US-09-396-196G-59362	Sequence 39362, A	c 180	5	US-09-640-211A-1871
	c 108	5	71.4	25	3	US-09-396-196G-59363	Sequence 39363, A	c 181	5	US-09-714-602-22
	c 109	5	71.4	25	3	US-09-396-196G-106891	Sequence 106891, A	c 182	5	US-09-313-294A-6624
	c 110	5	71.4	25	3	US-09-396-196G-118918	Sequence 118918, B	c 183	5	US-09-195-106-4
	c 111	5	71.4	27	3	US-09-57-79-41	Sequence 41, App1	c 184	5	US-09-880-107-126
	c 112	5	71.4	27	3	US-09-920-191A-41	Sequence 41, App1	c 185	5	US-09-880-107-294
	c 113	5	71.4	28	3	US-08-959-998-1084	Sequence 1084, App1	c 186	5	US-08-472-701-1
	c 114	5	71.4	28	3	US-09-225-228-1084	Sequence 1084, App1	c 187	5	US-08-589-028-3
	c 115	5	71.4	28	3	US-08-301B-1084	Sequence 1084, App1	c 188	5	US-09-328-701-1
	c 116	5	71.4	31	2	US-08-467-03-47	Sequence 47, App1	c 189	5	US-09-489-039A-3133
	c 117	5	71.4	31	2	US-08-466-193-47	Sequence 47, App1	c 190	5	US-09-107-532A-1827
	c 118	5	71.4	31	3	US-08-191-61A-47	Sequence 47, App1	c 191	5	US-09-583-110-29
	c 119	5	71.4	31	3	US-09-374-71A-47	Sequence 47, App1	c 192	5	US-08-943-607-47
	c 120	5	71.4	31	3	US-10-196-107A-47	Sequence 47, App1	c 193	5	US-08-589-028-3
	c 121	5	71.4	35	2	US-08-667-03-37	Sequence 37, App1	c 194	5	US-08-785-271-3
	c 122	5	71.4	35	2	US-08-466-93-37	Sequence 37, App1	c 195	5	US-09-974-300-7364
	c 123	5	71.4	35	2	US-08-467-03-47	Sequence 37, App1	c 196	5	US-09-640-211A-1956
	c 124	5	71.4	35	3	US-08-191-61A-47	Sequence 47, App1	c 197	5	US-09-640-211A-1956
	c 125	5	71.4	35	3	US-10-196-107A-37	Sequence 47, App1	c 198	5	US-09-973-278-826
	c 126	5	71.4	36	3	US-09-225-228-1084	Sequence 1084, App1	c 199	5	US-09-973-278-826
	c 127	5	71.4	46	3	US-08-503-37	Sequence 37, App1	c 200	5	US-09-605-703B-1833
	c 128	5	71.4	46	3	US-08-466-516-20	Sequence 20, App1	c 202	5	US-08-945-140-5
	c 129	5	71.4	46	3	US-08-837-034-20	Sequence 20, App1	c 203	5	US-09-640-1573-47
	c 130	5	71.4	46	3	US-09-136-801-32	Sequence 32, App1	c 204	5	US-09-713-501-47
	c 131	5	71.4	46	3	US-09-202-088A-32	Sequence 32, App1	c 205	5	US-09-825-294-47
	c 132	5	71.4	50	3	US-10-131-827-772	Sequence 772, App1	c 206	5	US-09-970-966-47
	c 133	5	71.4	71	7	PCT-US6-09337-43	Sequence 204, App1	c 207	5	US-09-513-999C-28470
	c 134	5	71.4	56	3	US-10-014-012-204	Sequence 204, App1	c 208	5	US-09-621-976-10758
	c 135	5	71.4	66	3	US-09-625-188-44	Sequence 43, App1	c 209	5	US-09-902-540-731
	c 136	5	71.4	71	3	US-08-481-710-43	Sequence 43, App1	c 210	5	US-09-323-738-1
	c 137	5	71.4	71	3	US-09-513-999C-28873	Sequence 28873, A	c 211	5	US-09-323-738-1
	c 138	5	71.4	79	3	US-09-433-826B-304	Sequence 43, App1	c 212	5	US-09-323-738-1
	c 139	5	71.4	79	3	US-10-131-821-772	Sequence 204, App1	c 213	5	US-09-323-738-1
	c 140	5	71.4	79	3	US-09-807-519-2	Sequence 304, App1	c 214	5	US-09-323-738-1
	c 141	5	71.4	79	3	US-09-289-681-304	Sequence 304, App1	c 215	5	US-09-323-738-1
	c 142	5	71.4	79	3	US-09-220-005B-304	Sequence 304, App1	c 216	5	US-09-323-738-1
	c 143	5	71.4	79	3	US-09-339-338-304	Sequence 304, App1	c 217	5	US-09-323-738-1
	c 144	5	71.4	79	3	US-09-433-826B-304	Sequence 304, App1	c 218	5	US-09-323-738-1
	c 145	5	71.4	79	3	US-09-004-087A-104	Sequence 304, App1	c 219	5	US-09-323-738-1
	c 146	5	71.4	79	3	US-09-834-559-304	Sequence 304, App1	c 220	5	US-09-323-738-1
	c 147	5	71.4	79	3	US-09-590-651A-204	Sequence 304, App1	c 221	5	US-09-323-738-1
	c 148	5	71.4	79	3	US-09-551-521A-104	Sequence 304, App1	c 222	5	US-09-323-738-1
	c 149	5	71.4	79	3	US-09-551-521A-104	Sequence 304, App1	c 223	5	US-09-323-738-1
	c 150	5	71.4	79	3	US-10-076-622-304	Sequence 304, App1	c 224	5	US-09-323-738-1
	c 151	5	71.4	79	4	US-10-124-805-304	Sequence 304, App1	c 225	5	US-09-323-738-1
	c 152	5	71.4	121	3	US-09-818-875-514	Sequence 513, App1	c 226	5	US-09-323-738-1
	c 153	5	71.4	121	3	US-09-818-875-514	Sequence 514, App1	c 227	5	US-09-323-738-1

Result No.	Query	Match Length	DB ID	Description
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1	7 100.0	21	12 ADQ16436	Adq16436 Nucleic acid
2	7 100.0	2000	8 ADT73402	Adt73402 Rice gene
3	6 85.7	48	6 ABN71781	Abn71781 Streptococcus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
<hr/>					
1	7	7 100.0	21	12 ADQ16436	Adq16436 Nucleic acid
2	7	7 100.0	2000	8 ADT73402	Adt73402 Rice gene
3	6	6 85.7	48	6 ABN71781	Abn71781 Streptococcus

77	85.7	2178	9	ADB08415	Alloiccoc	150	85.7	16555	4	AAK70102	Human imm
78	85.7	2178	9	ADB08417	Alloiccoc	151	85.7	19969	4	AAK65309	Human imm
79	85.7	2178	9	ADB08413	Alloiccoc	152	85.7	20598	4	AAE24851	Nucleotid
80	85.7	2209	4	AHH17074	Human CDN	153	85.7	20598	6	AAE24851	Nucleotid
81	85.7	2209	13	ADQ87393	Human tum	154	85.7	20598	6	AAE42515	Human zai
C 82	85.7	2215	4	AHH1419	Human CDN	155	85.7	23885	4	AAK73173	Human imm
C 83	85.7	2232	6	ABK35916	CDNA sequ	156	85.7	23885	4	AAK70103	Human imm
C 84	85.7	2383	4	AAB193833	Human pol	c 157	85.7	23885	4	AAK65726	Human imm
C 85	85.7	2386	4	AAB179667	Human CDN	c 158	85.7	23993	12	ADK16022	Human mam
C 86	85.7	2566	4	AAB179667	Human CDN	c 159	85.7	27150	4	ADD02701	Human gly
C 87	85.7	2569	10	ADC30561	Novel nov	c 160	85.7	27150	4	AAK70187	Human imm
93	85.7	2607	12	ADQ67217	Novel hum	c 161	85.7	27976	4	AAK79311	Human imm
C 94	85.7	2659	9	ABT43745	Molecule	c 162	85.7	32185	11	ACN44604	Mouse gen
C 95	85.7	2830	4	AAB158734	Human pol	c 163	85.7	32189	10	AAB10115	Human lun
C 96	85.7	2830	12	ADL26551	Human SE2	c 164	85.7	32189	10	ABd33452	Human nov
C 97	85.7	2867	6	ABN84190	Human cel	c 170	85.7	32189	10	AAB15153	Human sec
98	85.7	2872	5	ADQ98954	DNA encod	c 171	85.7	44615	10	ADb33407	Human kin
99	85.7	2902	3	AAC46853	Arabidops	c 172	85.7	44615	12	ADQ97551	Mouse can
100	85.7	3256	5	ADL45276	Human ova	c 173	85.7	44728	13	ABD32556	Mouse can
C 101	85.7	3289	8	ABX34745	Human mdd	c 174	85.7	51157	13	ABD32986	Mouse can
C 102	85.7	3324	6	AAS94913	Human tum	c 175	85.7	52746	13	AAb61129	Human FLJ
C 103	85.7	3339	13	ACN38144	Tumour-as	c 176	85.7	54732	13	ABD33335	Human can
C 104	85.7	3454	6	ADM9346	Mouse lym	c 177	85.7	58922	13	ABD33407	Human can
C 105	85.7	3454	6	ADD41009	Mouse PIJ	c 178	85.7	62658	13	ABD33339	Human can
C 106	85.7	3454	6	ABR72319	DNA encod	c 179	85.7	63105	13	ABD33339	Human can
C 107	85.7	3454	6	ABK72292	Lymphona	c 180	85.7	63294	9	ADA02939	Mouse Tle
C 108	85.7	3454	9	ABSS54198	Mouse CDN	c 181	85.7	63294	10	ADb72777	Mouse Tle
C 109	85.7	3454	12	ADM79346	Mouse PIk	c 182	85.7	63294	12	ADM74534	Murine ca
C 110	85.7	3454	10	ADB72666	Mouse PIk	c 183	85.7	63828	11	ACN44106	Human gen
C 111	85.7	3454	12	ADM79473	Mouse lym	c 184	85.7	74788	6	ACN45118	Human gen
C 112	85.7	3454	12	ADM79473	Murine ca	c 185	85.7	86431	6	Abd33213	Murine ca
C 113	85.7	3454	12	ADM60051	CRH signa	c 186	85.7	86431	6	AbD85419	Continuation (8 of
C 114	85.7	3454	12	ADM02928	Mouse PIk	c 187	85.7	86765	10	ADD14752	Human src
C 115	85.7	3454	10	ADB72666	Mouse PIk	c 188	85.7	86765	14	AEd17778	Fibrotic
C 116	85.7	3454	10	ADC85408	Mouse PIk	c 189	85.7	92726	9	ADA02927	Mouse Pik
C 117	85.7	3454	12	ADM79473	Mouse lym	c 190	85.7	92726	10	ABD72665	Mouse Pik
C 118	85.7	3454	12	ADM79473	Murine ca	c 191	85.7	92726	10	ADC85407	Mouse Pik
C 119	85.7	3454	12	ADM60051	CRH signa	c 192	85.7	92726	12	ADM74522	Murine ca
C 120	85.7	3729	13	ADM06678	Full leng	c 193	85.7	93538	13	ABD33442	Murine ca
C 121	85.7	3729	13	ADM14933	Plant CDN	c 194	85.7	94750	4	AEd2290	Genomic f
C 122	85.7	3999	2	AAX28025	Human lym	c 195	85.7	96988	3	AAX2290	BAc conta
C 123	85.7	3999	4	AAX29756	Human lym	c 196	85.7	99916	6	ADi03931	Human enz
C 124	85.7	4034	4	ABL09373	Drosophil	c 197	85.7	99916	6	ADi03931	Continuation (4 of
C 125	85.7	5139	4	ABL09373	Drosophil	c 198	85.7	110000	9	ABD12064	Continuation (7 of
C 126	85.7	5231	4	ABL14230	Drosophil	c 199	85.7	110000	9	ADb13435	Continuation (5 of
C 127	85.7	5245	5	ABL85296	DNA encod	c 200	85.7	110000	14	ADZ13575	Continuation (10 o
C 128	85.7	5245	5	ABL09460	Human cdn	c 201	85.7	110000	14	AED76254	Continuation (4 of
C 129	85.7	5367	6	ABL44190	Human lym	c 202	85.7	110000	14	AEB05138	Continuation (4 of
C 130	85.7	5367	7	ADM09461	Drosophil	c 203	85.7	116297	12	ADQ9758	Human can
C 131	85.7	5379	6	ADM09461	Drosophil	c 204	85.7	117574	6	AAU145288	Human KCN
C 132	85.7	5379	6	ADM09461	Drosophil	c 205	85.7	1262656	11	ACN44602	Human gen
C 133	85.7	5666	14	AEA19331	Novel hum	c 206	85.7	126990	12	ADP13332	Renal cel
C 134	85.7	5666	14	AED104221	Drosophil	c 207	85.7	128963	12	ADQ7110	Human can
C 135	85.7	5666	14	AED18331	Fibrotic	c 213	85.7	132050	11	ACN3912	Human gen
C 136	85.7	5924	6	ABq80570	Mutant hu	c 214	85.7	132762	10	ADH63063	Human fib
C 137	85.7	5924	6	ABq80569	Human che	c 215	85.7	140342	14	ADZ13043	Human can
C 138	85.7	5924	8	ACD13384	Human DNA	c 210	85.7	180283	14	AED18452	Fibrotic
C 139	85.7	6025	4	AAS45339	Chemical	c 211	85.7	193672	10	ADb113570	Osteoarth
C 140	85.7	6025	5	ABL14245	Drosophil	c 212	85.7	231222	10	ADb113593	Osteoarth
C 141	85.7	6025	6	ABq80570	Mutant p8	c 213	85.7	233060	11	ACN3912	Human gen
C 142	85.7	6025	10	ADE47336	Human car	c 209	85.7	242496	14	ADb76150	Mouse CA
C 143	85.7	6025	13	ADJ08754	Human car	c 210	85.7	254481	12	ADQ97135	Mouse can
C 144	85.7	6279	4	ABL14245	Drosophil	c 211	85.7	257645	12	ADQ97289	Human can
C 145	85.7	6279	4	ABL84202	Aspergill	c 212	85.7	349980	5	AHH65531	Ahh4966
C 146	85.7	6279	4	AAB1868	Human imm	c 213	85.7	349980	5	AHH6496	C glutami
C 147	85.7	9702	4	AAK70186	Human imm	c 214	85.7	349980	19	ADT15682	Ahh4966
C 148	85.7	11348	13	AAB84045	Human imm	c 215	85.7	349980	19	ADT8300	Human apo
C 149	85.7	11350	4	AAB84047	Human imm	c 216	85.7	349980	19	ADT82743	Apolipop
C 150	85.7	16555	4	AAB179667	Human imm	c 217	85.7	349980	19	ADT80125	Apolipop



c 77	85.7	326	5	HSRPS26D	X79236 Homo sapien	AB055923 Human ech	85.7	903	10
c 78	85.7	334	7	BY244336	SV234P226F	AB055924 Human ech	85.7	903	10
c 79	85.7	334	7	CC441235	Sequence	AF261151 Vibrio ch	85.7	927	15
c 80	85.7	376	11	CO441235	Sequence	CQ731389 Sequence	85.7	927	15
c 81	85.7	391	11	PCMSAT6FRR	Y12771 Phalacrocor	AF490530 Lycopersi	85.7	1021	2
c 82	85.7	391	2	AR210429	AX210429 Sequence	CS211757 Sequence	85.7	1038	4
c 83	85.7	447	2	AR443227	AR443227 Sequence	US1240 Cricetus	85.7	1084	6
c 84	85.7	448	2	CQ775557	CQ775557 Sequence	AY157969 Rattus no	85.7	1086	6
c 85	85.7	448	7	HSC11H04	AL152267 H. sapiens	AR375733 Sequence	85.7	1116	2
c 86	85.7	461	2	CQ21909	CQ921909 Sequence	AX654406 Sequence	85.7	1116	2
c 87	85.7	469	2	CQ295969	AY598732 Eulalia v	AR37535 Sequence	85.7	1128	2
c 88	85.7	477	13	AY598732	G34628 human SRS	CR350914 Gallus ga	85.7	1142	11
c 89	85.7	480	7	G34628	G99807 S208P601FC	BX950293 Gallus ga	85.7	1198	11
c 90	85.7	491	7	G39807	AX988217 Sequence	AR10810 Sequence	85.7	1216	2
c 91	85.7	491	7	AX988217	AX988217 Sequence	U85211 Trichromo	85.7	1250	13
c 92	85.7	497	2	BD123076	BD123076 EST and e	X05260 Mouse y chr	85.7	1285	6
c 93	85.7	497	2	AR425253	Sequence	AY617385 Sterkeli	85.7	1321	13
c 94	85.7	511	7	BV292235	BV292235 Sequence	AY377346 Gulo gulo	85.7	1378	14
c 95	85.7	517	2	BD151138	BD151138 Primer fo	AF100647 Trypanoso	85.7	1380	13
c 96	85.7	517	2	CQ717985	CQ717985 Sequence	AX025512 Sequence	85.7	1436	12
c 97	85.7	517	2	AX871076	AX871076 Sequence	U63308 Human eukar	85.7	1452	5
c 98	85.7	541	2	AX210455	AX210455 Sequence	D00564 Oryza sativ	85.7	1485	4
c 99	85.7	553	7	G90457	G90457 S208P641.6RE	AX463562 Sequence	85.7	1539	6
c 100	85.7	566	7	BV10893	BV10893 MARC 4607	X16153 Rice mtch	85.7	1546	4
c 101	85.7	566	2	CQ101506	CQ101506 Sequence	BD160574 Primer fo	85.7	1591	2
c 102	85.7	574	2	CO140501	CO140501 Sequence	AX883862 Sequence	85.7	1591	2
c 103	85.7	574	2	CO223819	CO223819 Sequence	AK024303 Homo sapi	85.7	170	6
c 104	85.7	574	2	CQ261806	CQ261806 Sequence	E64409 Peptid hav	85.7	171	6
c 105	85.7	574	2	CQ299052	CQ299052 Sequence	AX210627 Sequence	85.7	172	6
c 106	85.7	574	2	CQ335968	CQ335968 Sequence	AB015345 Homo sapi	85.7	173	6
c 107	85.7	580	6	IMN050414	U50414 Mus musculu	DC043226 Arabidops	85.7	174	6
c 108	85.7	589	7	BV356736	BV356736 S231P68R	BC032406 Homo sapi	85.7	175	6
c 109	85.7	596	6	AB0318243	AB0318243 Mus muscu	BC0343226 Homo sapi	85.7	176	6
c 110	85.7	613	7	BV068685	BV068685 S212P320	BC079216 Rattus no	85.7	177	6
c 111	85.7	632	7	BV356359	BV356359 S231P201	BD160575 Homo sapi	85.7	178	6
c 112	85.7	660	2	BD162334	BD162334 Novel pol	AY00295 Drosophil	85.7	179	6
c 113	85.7	660	2	AX120197	AX120197 Sequence	BC024183 Homo sapi	85.7	180	6
c 114	85.7	669	7	BV078027	BV078027 S212P035	BC034491 Homo sapi	85.7	181	6
c 115	85.7	672	2	AR764881	AR764881 Sequence	LA7271 Encephalo	85.7	182	13
c 116	85.7	681	2	BD149055	BD149055 Primer fo	AB016768 Mus muscu	85.7	1829	13
c 117	85.7	681	2	AX868993	AX868993 Sequence	AC111124 Bos tauru	85.7	1834	6
c 118	85.7	691	14	D0218446	DQ28446 Sus scrofa	BC026782 Homo sapi	85.7	1848	14
c 119	85.7	693	7	BV252516	BV252516 S234P375	BD159569 Primer fo	85.7	185	5
c 120	85.7	710	14	BV501024	S222P206	AX882860 Sequence	85.7	1856	13
c 121	85.7	724	10	AB167995	AB167995 Human ech	AK023362 Homo sapi	85.7	188	2
c 122	85.7	726	11	CAM90505	AJ290505 Carilia am	AK023362 Homo sapi	85.7	189	6
c 123	85.7	730	11	BX930880	BX930880 Gallus ga	AK023362 Homo sapi	85.7	190	6
c 124	85.7	738	7	BX933282	BX933282 Gallus ga	AK023362 Homo sapi	85.7	191	6
c 125	85.7	746	11	BX933282	BX933282 Gallus ga	AK023362 Homo sapi	85.7	191	6
c 126	85.7	749	7	BV656636	BD220724 Human gen	AK056166 Homo sapi	85.7	192	6
c 127	85.7	804	5	HSA324854	AJ324854 Homo sapi	AK0509675 Sequence	85.7	193	6
c 128	85.7	804	7	BV483129	BV483129 S1x14F53	BD159066 Primer fo	85.7	195	6
c 129	85.7	814	7	BV649478	BV649478 S216P6142	BC076289 Danio rer	85.7	207	6
c 130	85.7	815	4	AF162210	AF162210 Lactuca s	BC051105 Mus muscu	85.7	208	6
c 131	85.7	836	7	BV612195	BV612195 S217P6150	AK021622 Homo sapi	85.7	209	5
c 132	85.7	837	7	BV618122	BV618122 S217P6186	BD157411 Primer fo	85.7	210	6
c 133	85.7	846	6	BC054440	BC054440 Mus musculu	AX882860 Sequence	85.7	205	6
c 134	85.7	846	7	BV649478	BV649478 S215P6147	AK021844 Homo sapi	85.7	211	5
c 135	85.7	883	11	SV234P226F	SV234P226F	BD159066 Primer fo	85.7	213	6
c 136	85.7	883	11	SV234P226F	SV234P226F	BC076289 Danio rer	85.7	214	6
c 137	85.7	883	11	SV234P226F	SV234P226F	BC051105 Mus muscu	85.7	215	6
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c 141	85.7	883	11	SV234P226F	SV234P226F	AK021622 Homo sapi	85.7	219	6
c 142	85.7	883	11	SV234P226F	SV234P226F	BD159066 Primer fo	85.7	220	6
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c 147	85.7	883	11	SV234P226F	SV234P226F	AK021622 Homo sapi	85.7	225	6
c 148	85.7	883	11	SV234P226F	SV234P226F	BD159066 Primer fo	85.7	226	6
c 149	85.7	883	11	SV234P226F	SV234P226F	BC051105 Mus muscu	85.7	227	6

Result No.	Score	Query Match	Length	DB ID	Description
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1	37	100.0	21	6	US-10-537-648-28
2	34	91.9	864	8	US-11-266-748A-369840
c 3	34	91.9	864	8	US-11-266-748A-453019
c 4	34	91.9	59637	7	US-11-299-286-4370
c 5	34	91.9	59637	6	US-10-539-228-311
c 6	34	91.9	124074	8	US-11-266-748A-28242
c 7	34	91.9	128963	6	US-10-540-898-86

GenCore version 5.1.9  
(c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 12, 2006 20:46:38 (without alignments)

119.628 Million cell updates/sec  
(without alignments)

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQQQS 7

Scoring table: BLOSUM62

Xgapop 10.0 Xgapext 0.5

Ygapop 10.0 Ygapext 0.5

Fgapop 6.0 Fgapext 7.0

Delop 6.0 Delext 7.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 4791040

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

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GenCore version 5.1.9  
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(without alignments)

88.613 Million cell updates/sec

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Searched: 18892170 seqs, 6143817638 residues

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Maximum Match 100\*

Listing First 1000 summaries

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c 133	89.2	733	6	US-10-027-632-249885	Sequence 249885,	Sequence 326, App
c 134	89.2	733	7	US-10-027-632-249885	Sequence 249885,	Sequence 326, App
c 135	89.2	733	12	US-10-027-632-173565	Sequence 173565,	Sequence 326, App
c 136	89.2	733	12	US-10-027-632-173566	Sequence 173566,	Sequence 326, App
c 137	89.2	771	4	US-09-925-065A-6799	Sequence 6799, App	Sequence 326, App
c 138	89.2	771	5	US-09-925-065A-6799	Sequence 6799, App	Sequence 326, App
c 139	89.2	771	12	US-10-027-632-173567	Sequence 173567,	Sequence 326, App
c 140	89.2	771	12	US-10-027-632-173567	Sequence 173567,	Sequence 326, App
c 141	89.2	802	6	US-10-027-632-173568	Sequence 173568,	Sequence 326, App
c 142	89.2	802	6	US-10-027-632-173568	Sequence 173568,	Sequence 326, App
c 143	89.2	802	7	US-10-027-632-173569	Sequence 173569,	Sequence 326, App
c 144	89.2	802	7	US-10-027-632-173569	Sequence 173569,	Sequence 326, App
c 145	89.2	806	6	US-10-027-632-152361	Sequence 152361,	Sequence 326, App
c 146	89.2	806	6	US-10-027-632-152361	Sequence 152361,	Sequence 326, App
c 147	89.2	806	7	US-10-027-632-152361	Sequence 152361,	Sequence 326, App

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1	34	91.9	892	3	US-09-533-559-532	Sequence 532, App
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C 3	33	89.2	601	3	US-09-949-016-41638	Sequence 44638, A
C 4	33	89.2	601	3	US-09-949-016-70938	Sequence 76038, A
5	33	89.2	601	3	US-09-949-016-184545	Sequence 184545, A
6	33	89.2	601	3	US-09-949-016-184546	Sequence 184546, A
C 7	33	89.2	1116	3	US-09-543-881A-739	Sequence 739, App
C 8	33	89.2	1216	3	US-09-838-151A-62	Sequence 62, App

82	31	83.8	21000	3	US-09-975-123-11	Sequence 11, App1	155	81.1	958	3	US-09-533-559-5090
83	31	83.8	21048	3	US-09-949-016-12480	Sequence 1601, A	c 156	81.1	1020	4	US-09-973-543-681A-41
c 84	31	83.8	21170	3	US-09-949-016-12480	Sequence 1240, A	c 157	81.1	1128	3	US-09-949-039A-41
c 85	31	83.8	22908	3	US-09-949-016-1255	Sequence 1725, A	c 158	81.1	1266	3	US-09-489-039A-2484
c 86	31	83.8	27630	3	US-09-949-016-15362	Sequence 1632, A	c 159	81.1	1368	3	US-09-248-796A-2395
c 87	31	83.8	40576	3	US-09-949-016-12329	Sequence 12329, A	c 160	81.1	1587	3	US-09-712-363-48
c 88	31	83.8	40577	3	US-09-949-016-16663	Sequence 16663, A	c 161	81.1	1588	3	US-09-490-291-7
c 89	31	83.8	48994	3	US-09-949-016-16091	Sequence 14091, A	c 162	81.1	1852	3	US-09-485-452-4
c 90	31	83.8	58543	3	US-09-949-016-15565	Sequence 13595, A	c 163	81.1	1922	2	US-08-372-652-9
c 91	31	83.8	63154	3	US-09-949-016-14025	Sequence 14095, A	c 164	81.1	1922	7	PCT-US95-16311-9
c 92	31	83.8	65192	3	US-09-949-002-31	Sequence 31, App1	c 165	81.1	2047	3	US-09-270-77-11235
c 93	31	83.8	119153	3	US-09-949-016-12378	Sequence 12378, A	c 172	81.1	2166	3	US-09-248-796A-2394
c 94	31	83.8	119762	3	US-09-949-016-17313	Sequence 17313, A	c 173	81.1	2179	3	US-10-138-075-3
c 95	31	83.8	193303	3	US-09-949-016-15561	Sequence 14495, A	c 168	81.1	2338	2	US-08-425-669-1
c 96	31	83.8	193303	3	US-09-949-016-15561	Sequence 14091, A	c 169	81.1	2338	2	US-08-31-844B-1
c 97	31	83.8	199933	3	US-09-949-016-14172	Sequence 14122, A	c 170	81.1	2812	3	US-09-620-312D-624
c 98	31	83.8	196714	3	US-09-949-016-15747	Sequence 15474, A	c 171	81.1	2970	3	US-09-805-594B-7
c 99	31	83.8	197131	3	US-09-949-016-12675	Sequence 12675, A	c 172	81.1	3018	3	US-09-949-016-1097
c 100	31	83.8	197132	3	US-09-949-016-12170	Sequence 17132, A	c 173	81.1	3018	3	US-09-949-016-14749
c 101	31	83.8	201093	3	US-09-949-016-1445	Sequence 1445, A	c 174	81.1	3018	3	US-09-689-486-4
c 102	31	83.8	250598	3	US-09-949-016-16061	Sequence 16061, A	c 175	81.1	3018	4	US-09-973-424A-4
c 103	31	83.8	331814	3	US-09-949-016-12008	Sequence 12008, A	c 176	81.1	4871	3	US-09-799-451-448
c 104	31	83.8	331814	3	US-09-949-016-17056	Sequence 17056, A	c 177	81.1	5345	2	US-08-044-618-7
c 105	31	83.8	421118	3	US-09-949-016-12675	Sequence 16297, A	c 178	81.1	7179	3	US-09-949-016-12365
c 106	30	81.1	215	3	US-09-949-016-12170	Sequence 13682, A	c 179	81.1	7780	3	US-09-632-033B-2
c 107	30	81.1	239	3	US-09-949-016-1445	Sequence 23164, A	c 180	81.1	7912	3	US-09-949-016-3804
c 108	30	81.1	289	3	US-09-949-016-16061	Sequence 1983, A	c 181	81.1	7940	3	US-09-632-033B-1
c 109	30	81.1	447	3	US-09-949-016-12008	Sequence 12008, A	c 182	81.1	10143	3	US-09-15481
c 110	30	81.1	497	3	US-09-949-016-14172	Sequence 14122, A	c 183	81.1	10183	3	US-09-949-016-13111
c 111	30	81.1	601	3	US-09-949-016-12029	Sequence 2776, A	c 184	81.1	11122	5	US-09-984-429-194
c 112	30	81.1	601	3	US-09-949-016-13682	Sequence 30525, A	c 185	81.1	11122	5	US-09-984-429-144
c 113	30	81.1	601	3	US-09-949-016-15134	Sequence 23164, A	c 186	81.1	16505	3	US-09-949-016-11962
c 114	30	81.1	601	3	US-09-949-016-299A-1983	Sequence 37188, A	c 187	81.1	20598	3	US-09-949-016-13836
c 115	30	81.1	601	3	US-09-949-016-12008	Sequence 46890, A	c 188	81.1	21952	3	US-09-949-016-12110
c 116	30	81.1	601	3	US-09-949-016-15747	Sequence 19050, A	c 189	81.1	21953	3	US-09-949-016-15795
c 117	30	81.1	601	3	US-09-949-016-12766	Sequence 17056, A	c 190	81.1	21983	3	US-09-984-429-194
c 118	30	81.1	601	3	US-09-949-016-10525	Sequence 68477, A	c 191	81.1	19826	3	US-09-949-016-16973
c 119	30	81.1	601	3	US-09-949-016-3714	Sequence 37188, A	c 192	81.1	20598	3	US-09-949-016-13836
c 120	30	81.1	601	3	US-09-949-016-3714	Sequence 8571, A	c 193	81.1	20598	3	US-10-139-667-10
c 121	30	81.1	601	3	US-09-949-016-48880	Sequence 46890, A	c 194	81.1	20662	3	US-09-949-016-1717
c 122	30	81.1	601	3	US-09-949-016-52559	Sequence 52559, A	c 195	81.1	21360	3	US-09-949-016-12857
c 123	30	81.1	601	3	US-09-949-016-27766	Sequence 68133, A	c 196	81.1	21361	3	US-09-949-016-16245
c 124	30	81.1	601	3	US-09-949-016-68477	Sequence 68477, A	c 197	81.1	27783	3	US-09-593-828-20
c 125	30	81.1	601	3	US-09-949-016-68478	Sequence 68478, A	c 198	81.1	27783	3	US-09-949-016-16736
c 126	30	81.1	601	3	US-09-949-016-15734	Sequence 11527,	c 199	81.1	28198	3	US-09-949-016-12349
c 127	30	81.1	601	3	US-09-949-016-115827	Sequence 103077,	c 200	81.1	28596	3	US-09-949-016-16887
c 128	30	81.1	601	3	US-09-949-016-10152	Sequence 10352,	c 201	81.1	30656	3	US-09-949-016-1428
c 129	30	81.1	601	3	US-09-949-016-115548	Sequence 11548,	c 202	81.1	31545	3	US-09-949-016-16248
c 130	30	81.1	601	3	US-09-949-016-115641	Sequence 11541,	c 203	81.1	36611	3	US-09-593-828-20
c 131	30	81.1	601	3	US-09-949-016-116199	Sequence 11699,	c 204	81.1	42376	3	US-09-949-016-16726
c 132	30	81.1	601	3	US-09-949-016-116292	Sequence 11699,	c 205	81.1	42741	3	US-09-949-016-12957
c 133	30	81.1	601	3	US-09-949-016-115920	Sequence 11520,	c 206	81.1	42989	3	US-09-949-016-12291
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c 135	30	81.1	601	3	US-09-949-016-116106	Sequence 116106,	c 208	81.1	44291	3	US-09-949-016-15428
c 136	30	81.1	601	3	US-09-949-016-116199	Sequence 11699,	c 209	81.1	44314	3	US-09-949-016-17287
c 137	30	81.1	601	3	US-09-949-016-116292	Sequence 11699,	c 210	81.1	44345	3	US-09-949-016-16491
c 138	30	81.1	601	3	US-09-949-016-116385	Sequence 11685,	c 211	81.1	43950	3	US-10-060-322-3
c 139	30	81.1	601	3	US-09-949-016-122735	Sequence 13235,	c 212	81.1	43950	3	US-10-339-657-3
c 140	30	81.1	601	3	US-09-949-016-132736	Sequence 13236,	c 213	81.1	53769	3	US-09-949-016-15227
c 141	30	81.1	601	3	US-09-949-016-132737	Sequence 13237,	c 214	81.1	44821	3	US-09-949-016-15227
c 142	30	81.1	601	3	US-09-949-016-132738	Sequence 13238,	c 215	81.1	46499	3	US-09-949-016-14032
c 143	30	81.1	601	3	US-09-949-016-132739	Sequence 13239,	c 216	81.1	47677	3	US-09-949-016-16491
c 144	30	81.1	601	3	US-09-949-016-132740	Sequence 13239,	c 217	81.1	50368	3	US-09-949-016-13256
c 145	30	81.1	601	3	US-09-949-016-146130	Sequence 146130,	c 218	81.1	51252	3	US-09-949-016-16348
c 146	30	81.1	601	3	US-09-949-016-146319	Sequence 146319,	c 219	81.1	53769	3	US-09-949-016-15227
c 147	30	81.1	601	3	US-09-949-016-146322	Sequence 146322,	c 220	81.1	58789	3	US-09-949-016-15922
c 148	30	81.1	601	3	US-09-949-016-148719	Sequence 148719,	c 221	81.1	69752	3	US-09-949-016-14094
c 149	30	81.1	601	3	US-09-949-016-166659	Sequence 166659,	c 222	81.1	77752	3	US-09-949-016-17417
c 150	30	81.1	601	3	US-09-949-016-166659	Sequence 166659,	c 223	81.1	77997	3	US-09-949-016-12249
c 151	30	81.1	601	3	US-09-949-016-168653	Sequence 168653,	c 224	81.1	80858	3	US-09-949-016-12659
c 152	30	81.1	601	3	US-09-949-016-187964	Sequence 187964,	c 225	81.1	80858	3	US-09-949-016-15715
c 153	30	81.1	601	3	US-09-949-016-187964	Sequence 187964,	c 226	81.1	88036	3	US-09-949-016-15335
c 154	30	81.1	601	3	US-09-949-016-187964	Sequence 187964,	c 227	81.1	90618	3	US-09-949-016-15964

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 12, 2005, 20:44:55 (without alignments) 188.674 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Egapop 6.0 , Egapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27953665780 residues

Total number of hits satisfying chosen Parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 1000 summaries

Command line parameters:

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-MODEL=frame+_p2n model -DEV=1h
-Q=/absbs/ABSSWBS/spool/US10537648/runat_12102006_151428_15082/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=pin.rst -MINMATCH=0.1 -LOOPPEXT=0
-UNITS=bits -START=1 -END=1 -MATTRX=blobsum62 -TRANS=human40 cdi -LISN=1000
-DCAALIGN=200 -THR SCORE=-MAXR=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=1000 -HOST=absbs3h
-USER=US10537648 @CGN_1_1_6323 @runat_12102006_151428_15082 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT=30 -DSPBLOCK=10 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -KGAPOP=10 -XGAPEXT=7 -FGAPEXT=6 -FGAPOP=6 -FRGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
  
```

Database : EST :

- 1: 9b\_est1:\*
- 2: 9b\_est3:\*
- 3: 9b\_est4:\*
- 4: 9b\_est5:\*
- 5: 9b\_est6:\*
- 6: 9b\_htc:\*
- 7: 9b\_est2:\*
- 8: 9b\_est7:\*
- 9: 9b\_est8:\*
- 10: 9b\_est9:\*
- 11: 9b\_gbs1:\*
- 12: 9b\_gbs2:\*
- 13: 9b\_gbs3:\*
- 14: 9b\_gbs4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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c 3	37	100.0	320 12	CE833641 tigr_gbs-AZ240574 RPCI-23-7
c 4	37	100.0	331 11	AZ240574 RPCI-23-7

CG37923 OG0CP55TV CG237923 OG0CP55TV

BB358863 BB358863 AK200728 Mus muscu CE833641 tigr\_gbs-AZ240574 RPCI-23-7

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CZ638826 OM\_B0018

AO252207 HS\_3108\_A

DE130155 Orzytias\_1

CR176637 Reverse\_B

CR192824 Reverse\_B

AQ464802 HS\_5105\_B

CR261251 Reverse\_B

CR251702 Reverse\_B

BJ838064 BJ838064

BZ879825 CH240 293

BZ826782 BJ826782

BZ921378 CH240\_119

AQ077211 C1T-HSP-2

BJ830318 BJ830318

CR149426 Reverse\_B

AG494285 Mus muscu

BH595970 BOGVE11TF

BX9656213 Reverse\_B

CR130680 Reverse\_B

CT047189 Sus scrofa

BH064279 RPCI-24-3

CL831140 OR\_CB1005

CG671428 trs2160

AG865816 Orzyta sat

CC541008 CH240\_421

CG818959 SOYCD72TH

AG896133 Orzyta sat

AL277782 Tetraodon

CC93803 FUHDK10TD

CP492357 MG1-0045T

AV291967 AV291967

CG733995 1119161E1

CF493005 MS1-0131U

CF493257 MG1-0080T

CF492849 MS1-0063U

CF492337 MG1-0024U

CF492667 MG1-0014G

CF492331 MG1-016T

BI9277985 EST547862

CF492433 MG1-016T

CF492826 MS1-0050G

CF492873 MS1-0063U

CF492824 MS1-0060G

CF492825 MS1-0060G

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CP492077 MA3-9999U

CF493012 MS1-0132T

CF492583 MS1-0004T

CP492131 MG1-0006T

CE55160 tigr\_gbs-B

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BU283824 GO386799

CF492047 MA3-9999U

AG104428 Pan trogl

CG192771 PUGN337TB

CF492229 MB1-0038G

CG80520 QVND8837H

CP492057 MA3-9999U

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DV533421

BH201530

BZ734651

DV145071

DV533421

BZ734651

DV145668

BQ882260

DW145668 CLV10762

BQ882260 AGENCOURT

BZ734651

DW145071 CLV10139

DW071393 62293 Tom

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		BZ761974	SALK_0388		C 155	34	91.9	932	14	CNS057WM
		W79925	zdi4a05_r1		C 156	34	91.9	937	11	AZ631879
		AQ556108	HS_5223_B		C 157	34	91.9	973	7	BE739456
		CV071393	CS_gil_37		C 158	34	91.9	980	14	AL310446
		AA175629	ms96g05_r		C 159	34	91.9	1076	7	Retraction
		DB055884	Oryzias1		C 160	34	91.9	1076	7	CF241333
		BZ839488	2M0135F08		C 161	34	91.9	1361	10	DV798971
		BM421354	V008B04		C 162	34	91.9	1553	12	CC261-16N
		CZ637278	OM_-B018		C 163	33	89.2	1712	6	CCM80803
		AQ004550	CIT-HSP-2		C 164	33	89.2	162	3	BU034430
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		BO373222	QVI_-FT016		C 166	33	89.2	170	11	AZ221234
		CV973830	EST00168		C 170	33	89.2	172	10	DW364299
		AA177106	nc02d11_8		C 171	33	89.2	178	7	DFW34299_LRAGE097
		BF724407	bz0407_y		C 167	33	89.2	178	7	CF395118
		A2060026	RPCI-3-4		C 168	33	89.2	188	2	UI-R-CH0
		AQ881729	HS_5272_A		C 169	33	89.2	201	1	BM194524
		BX109157	BX109157_-		C 170	33	89.2	201	1	AL376500
		CV973830	EST00168		C 171	33	89.2	214	1	MBB22F10
		AA177106	nc02d11_8		C 172	33	89.2	222	14	AA977165
		BF724407	bz0407_y		C 173	33	89.2	229	1	DV48164
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		AA046904	zFe7d12_r		C 177	33	89.2	254	10	AV292176
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		AV810274	AV810274		C 182	33	89.2	288	2	BB292176
		DA888816	DA888816		C 183	33	89.2	288	4	BB292176
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		AA635507	n36a11_8		C 194	33	89.2	294	10	DU414893
		AA116422	DRF2P54_XG		C 195	33	89.2	294	10	DU414893
		BP382458	601815440		C 196	33	89.2	294	10	DU414893
		A2878051	RPCI-3-1		C 197	33	89.2	294	10	DU414893
		BBH4505	CH230-05B		C 198	33	89.2	294	10	DU414893
		CA066990	SCUFA0101		C 199	33	89.2	294	10	DU414893
		BM223856	UI_E-EO1-		C 200	33	89.2	324	1	BB292176
		AG063207	Pan_trog1		C 201	33	89.2	324	1	BB292176
		BJ625552	Bj725552		C 202	33	89.2	324	1	BB292176
		DY165808	OR_ABA002		C 203	33	89.2	324	1	BB292176
		BH833188	BAcPP4_N1		C 204	33	89.2	324	1	BB292176
		CD633617	AGRNCOU7		C 205	33	89.2	324	1	BB292176
		BK126995	Danio rer		C 206	33	89.2	324	1	BB292176
		DX015611	KSB001T0		C 207	33	89.2	324	1	BB292176
		CG133113	PuWFA03TID		C 208	33	89.2	324	1	BB292176
		AG103444	Pan_trog1		C 209	33	89.2	324	1	BB292176
		AG098613	Par_trog1		C 210	33	89.2	324	1	BB292176
		BF28958	AGRNCOU7		C 211	33	89.2	324	1	BB292176
		C2432372	Sub_scrof		C 212	33	89.2	324	1	BB292176
		BI165925	DB165925		C 213	33	89.2	324	1	BB292176
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		BI1652561	601299470		C 218	33	89.2	324	1	BB292176
		CG926946	t02d05ba		C 219	33	89.2	324	1	BB292176
		CR035156	Forward_S		C 220	33	89.2	324	1	BB292176
		CH968207	AIIA_aaa0		C 221	33	89.2	324	1	BB292176
		DN210104	Mebo0114		C 222	33	89.2	324	1	BB292176
		CDN216103	AGRNCOU7		C 223	33	89.2	324	1	BB292176
		CDN216104	AGRNCOU7		C 224	33	89.2	324	1	BB292176
		CDN216105	AGRNCOU7		C 225	33	89.2	324	1	BB292176

OM protein - nucleic search, using frame_plus_p2n mode]		Acc48787 Human Evi	
Copyright (c) 1993 - 2006 Biocceleration Ltd.		Adp45533 Human Rhodopsin	
Run on: October 12, 2006, 20:36:29 ; Search time 430 Seconds (without alignments)		Adp45533 Human Rhodopsin	
Result No.	Score	Query Match Length DB ID	Description
1	37	100.0	21 12 ADQ16436
2	37	100.0	2000 8 ADQ16436
3	94.6	16098	8 ACC48787 Human Evi
4	94.6	16098	8 ACC48787 Human Evi
5	94.6	147700	12 ADP45533 Human Rhodopsin
6	94.6	147700	14 ADX98570 Human Guanine
7	94.6	147700	15 AEE96613 KIAA0661
8	91.9	376	6 ABn19259 Human ORF
9	91.9	866	4 AAH34154 Human col
10	91.9	892	3 AAF08009 Fusarium
11	91.9	892	13 ADU52050 Fusarium
12	91.9	892	14 ADZ90053 Cotton CD
13	91.9	1026	13 ADR64766 Cotton CD
14	91.9	1354	6 ADR35925 cDNA seq
15	91.9	2000	6 ABZ16565 Arabidops
16	91.9	2000	8 ADA68927 Arabidops
17	91.9	2448	6 Abn79854 Fungal 2B
18	91.9	3953	13 ADT14953 Plant CDN
19	91.9	5379	6 ABL13230 Human immunoglobulin
20	91.9	529693	12 ADQ97110 Human can
21	91.9	1242916	14 AED76150 Mouse CA
22	91.9	295096	11 ACN44068 Mouse gene
23	91.9	121	10 ADH92944 Human gene
24	91.9	392	5 AHH81562 Human diff
25	89.2	411	13 ACF86753 Human SIR
26	89.2	492	13 ACF81501 Human SIR
27	89.2	492	13 ACF81501 Human SIR
28	89.2	584	10 ADK52888 Plant DNA
29	89.2	996	13 ADS45661 Plant DNA
30	89.2	1116	10 ADP0054 Bacterial
31	89.2	1216	2 AAT93320 Tomato-in
32	89.2	1333	10 ADB8504 Human GPC
33	89.2	1539	6 AAL48581 A. rhizian
34	89.2	1943	5 AAS45223 cDNA enc
35	89.2	2178	9 ADB08415 Alliococ
36	89.2	2178	9 ADB08417 Alliococ
37	89.2	2178	9 ADB08413 Alliococ
38	89.2	2569	10 ADC30221 Human novaezeae
39	89.2	2659	9 ADB08417 Alliococ
40	89.2	3324	6 AAS94913 Human DNA
41	89.2	3999	2 AAX28025 Human IKA
42	89.2	3999	4 AAF29756 Human IKA
43	89.2	4417	13 ADR07102 Full length
44	89.2	4779	4 ABL17932 Drosophil
45	89.2	4788	4 AHH14533 Human CDH
46	89.2	4803	5 AAH81767 Human dif
47	89.2	4803	6 AAL44190 Murant hu
48	89.2	5924	6 ABQ80570 Murant hu
49	89.2	5924	6 ABQ80569 Human IKB
50	89.2	5924	8 ACD13384 Human DNA
51	89.2	6696	6 AAS6320 Chimeric
52	89.2	7282	4 AAK86318 Human imm
53	89.2	7599	2 AAX58802 Human leu
54	89.2	8436	13 ADR48202 Aspergillus
55	89.2	18888	4 ABL23020 Drosophil
56	89.2	20689	4 AAK78366 Human imm
57	89.2	32185	11 ACN44644 Human gene
58	89.2	39325	4 AAK81660 Human imm
59	89.2	50460	11 ACN44916 Human gene
60	89.2	54735	13 AAS3335 Human gene
61	89.2	56153	4 AAS46793 Tumour su
62	89.2	58922	13 ABD33407 Human can
63	89.2	86434	10 ADL13570 Osteoarthritis
64	89.2	96988	3 AAF22280 BAC conta
65	89.2	110000	6 ABA90521-18
66	89.2	110000	9 ADB1204-06
67	89.2	110000	14 AEE05338-3
68	89.2	126990	12 ADP1332-3
69	89.2	194534	10 ADQ97481 Human can
70	89.2	216215	10 ADF69167 Human MP5
71	89.2	217409	11 ACN45150 Human gene
72	86.5	31	2 AAV59931 PCR Prime
73	86.5	31	2 AAV58465 Primer fo
74	86.5	31	2 AAV59931 PCR Prime
75	86.5	31	2 AAV59931 PCR Prime
SUMMARIES			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			

c	77	121	4	ABA77668	Retinobla	150	32	86.5	3555	2	AAV58440	Modified		
c	78	86.5	13	ADX12593	Plant ful	151	32	86.5	3765	14	AEC84737	Human cDN		
c	79	86.5	4	AB109413	Drosophil	152	32	86.5	3765	14	AEC84737	Human cDN		
c	80	32	86.5	576	12	ADQ34573	c	153	32	86.5	3877	12	ADP90661	Mouse ext
c	81	32	86.5	591	13	ACN60533	Human SLI	154	32	86.5	4432	13	ADP90661	Mouse ext
c	82	32	86.5	600	10	ACF68049	Photorhab	155	32	86.5	4579	1	AAN81261	Rat card
c	83	32	86.5	631	5	ABV50016	Human Pro	156	32	86.5	4597	1	AAN81369	Human ret
c	84	32	86.5	639	10	ABF00608	Bacteri	157	32	86.5	4597	2	AQ070536	Human ret
c	85	32	86.5	795	6	AB12201	Arabidops	158	32	86.5	4597	2	AAX04501	Human ret
c	86	32	86.5	1020	10	ADC92233	E. faeciu	159	32	86.5	4600	13	ADP52909	Drug ther
c	87	32	86.5	1024	10	AB28343	Toxicolog	160	32	86.5	4641	4	ABL6126	Drosophil
c	93	32	86.5	1056	3	AAC74383	Arabidops	161	32	86.5	4740	6	ABK86079	Human ret
c	94	32	86.5	1063	3	AAC33107	Arabidops	162	32	86.5	4740	10	ADP84952	Farnesyl
c	95	32	86.5	1125	8	AAC32019	Prokaryot	163	32	86.5	4740	10	ADK67029	Gene #119
c	96	32	86.5	1161	6	AB189390	Babesia m	164	32	86.5	4740	12	ADP21395	Gene RBL
c	97	32	86.5	1161	10	ABD06059	BMN1-rela	165	32	86.5	4740	14	ADY15003	DNA encod
c	98	32	86.5	1162	6	AB189383	Babesia m	166	32	86.5	4740	14	ADY19476	DNA encod
c	99	32	86.5	1162	10	ABD06052	BMN1-rela	167	32	86.5	4740	15	AEP7497	Human pol
c	100	32	86.5	1162	10	ABD06052	Babesia m	168	32	86.5	4741	12	ACF7516	Human Rb
c	101	32	86.5	1248	6	AB189429	Prokaryot	169	32	86.5	4839	3	AAB8844	Human and
c	102	32	86.5	1248	10	ACD06111	BMN1-rela	170	32	86.5	4839	3	AAB2391	Human ret
c	103	32	86.5	1304	13	ADT15452	Plant cDN	171	32	86.5	4839	6	ABL2873	Breast ca
c	98	32	86.5	1375	11	ADP65595	Human alP	172	32	86.5	4839	12	ADP72311	Human Rb
c	99	32	86.5	1904	13	ADT18553	Plant cDN	173	32	86.5	4839	12	ADT47406	Human pol
c	100	32	86.5	1974	8	ACM53600	Prokaryot	174	32	86.5	4839	15	AEP74994	Human pol
c	101	32	86.5	2263	14	AFA22558	Mouse LRM	175	32	86.5	5056	1	AAN90499	cDNA of h
c	102	32	86.5	2466	10	AB109412	Drosophil	176	32	86.5	5430	4	AAS44291	Tumour su
c	103	32	86.5	2787	14	AEC21579	Human ret	177	32	86.5	5884	6	ABL34164	Human imm
c	104	32	86.5	2824	14	AEB55595	Human ret	178	32	86.5	6301	6	ABL32052	Human imm
c	105	32	86.5	2994	2	AAQ04713	Cancer su	179	32	86.5	8690	4	ABL29150	Drosophil
c	106	32	86.5	2994	2	AAQ11545	Retinobla	180	32	86.5	12988	4	AAS36785	Human car
c	107	32	86.5	2994	2	Aav40004	Retinobla	181	32	86.5	12988	10	ADB47479	Human car
c	108	32	86.5	2994	2	Aaz4287	Wild type	182	32	86.5	12988	13	ADB08897	Human car
c	109	32	86.5	2994	10	ADE21373	Retinobla	183	32	86.5	18036	4	AAS36787	Human car
c	110	32	86.5	2994	14	AEB55599	Human ret	184	32	86.5	21803	10	ADE7481	Human car
c	111	32	86.5	2994	14	ADW20875	Retinobla	185	32	86.5	18036	13	ADJ08899	Human car
c	112	32	86.5	2994	15	AEF64205	Human ret	186	32	86.5	18177	1	AAN0490	cDNA of h
c	113	32	86.5	2995	2	AAQ09059	Retinobla	187	32	86.5	18303	2	AAX04502	Human ret
c	114	32	86.5	2995	2	AQ086398	Human Rb1	188	32	86.5	24993	4	AAK65726	Human imm
c	115	32	86.5	2995	2	AQX90350	Human P11	189	32	86.5	25373	12	ADK16022	Human imm
c	116	32	86.5	2995	12	ADP72347	CDNA enc	190	32	86.5	51469	4	AAK78813	Human imm
c	117	32	86.5	2995	2	AB1094094	Retinobla	191	32	86.5	51469	4	AAK7070	Human imm
c	118	32	86.5	2995	4	AHH25755	Retinobla	192	32	86.5	51469	4	AAK63322	Human imm
c	119	32	86.5	2995	5	ADD04474	Retinobla	193	32	86.5	51469	12	ADH54712	Human VEG
c	120	32	86.5	2995	9	ACD28570	Human ret	194	32	86.5	61020	4	AAS46788	Tumour su
c	121	32	86.5	2995	2	AQX90350	Human ret	195	32	86.5	80423	13	ABD12576	Mouse can
c	122	32	86.5	2995	2	AQX00737	CDNA enc	196	32	86.5	251469	4	AAK78813	Human imm
c	123	32	86.5	2995	14	AB1094094	Retinobla	197	32	86.5	92219	14	ADZ13328	Murine ca
c	124	32	86.5	2995	14	ADW20878	Retinobla	198	32	86.5	110000	10	ACR7367_07	Continuation (8 of
c	125	32	86.5	2995	5	ADD04474	Retinobla	199	32	86.5	110000	12	ACR045384	Continuation (2 of
c	126	32	86.5	2995	2	AQX90350	Modified	200	32	86.5	110000	12	ACD04435_2	Continuation (13 of
c	127	32	86.5	3196	8	ABX79049	Human ret	201	32	86.5	247544	12	ADQ59419	Human can
c	128	32	86.5	3218	2	AQX54991	DNA sequ	202	32	86.5	247544	14	ADZ13328	Murine ca
c	129	32	86.5	3233	2	AQX54991	Modified	203	31	83.8	47	3	AZB8963	Human map
c	130	32	86.5	3244	8	ABX79076	Human ret	204	31	83.8	60	3	Aco8933	Human sp1
c	131	32	86.5	3266	2	AQX58444	Modified	205	31	83.8	154	3	AAC09933	Human sec
c	132	32	86.5	3089	8	ABX79077	Human ret	206	31	83.8	223	2	AQG16451	Human gen
c	133	32	86.5	3113	2	AQX58445	Modified	207	31	83.8	353	4	AAB13377	Human bre
c	134	32	86.5	3299	8	ABX79078	Human ret	208	31	83.8	384	6	ABN25373	Human ORF
c	135	32	86.5	3323	2	AQX58445	Modified	209	31	83.8	634	6	ABN63462	Human can
c	136	32	86.5	3353	8	ABX79082	Human ret	210	31	83.8	387	5	AAC20823	Human sec
c	137	32	86.5	3347	8	ABX79083	Human ret	211	31	83.8	433	3	AAB13115	Human bre
c	138	32	86.5	3368	8	ABX79078	Human ret	212	31	83.8	456	4	AAC91110	Breast ca
c	139	32	86.5	3377	2	AQX58445	Modified	213	31	83.8	483	11	ACN91110	Human bre
c	140	32	86.5	3383	2	AQX58445	Modified	214	31	83.8	570	13	ADG49311	Novel can
c	141	32	86.5	3392	2	AQX58446	Modified	215	31	83.8	634	6	ABn3939	Human can
c	142	32	86.5	3433	8	ABX79073	Human ret	216	31	83.8	641	6	ABn63443	Human can
c	143	32	86.5	3437	8	ABX79079	Human ret	217	31	83.8	665	3	AAB33982	Mouse sec
c	144	32	86.5	3455	2	AQX58447	Modified	218	31	83.8	672	3	ACF5011	Human ORF
c	145	32	86.5	3461	2	AQX58447	Modified	219	31	83.8	672	6	ABn19222	Human ORF
c	146	32	86.5	3532	8	ABX79084	Human ret	220	31	83.8	707	6	ABT09038	Phase 1 R
c	147	32	86.5	3533	8	ABX79048	Human ret	221	31	83.8	774	6	ABK73492	Bacillus
c	148	32	86.5	3554	2	AQX58452	Modified	222	31	83.8	833	11	ACN83233	Breast ca
c	149	32	86.5	3555	2	AQX54990	DNA sequ	223	31	83.8	833	11	ACN83233	Breast ca